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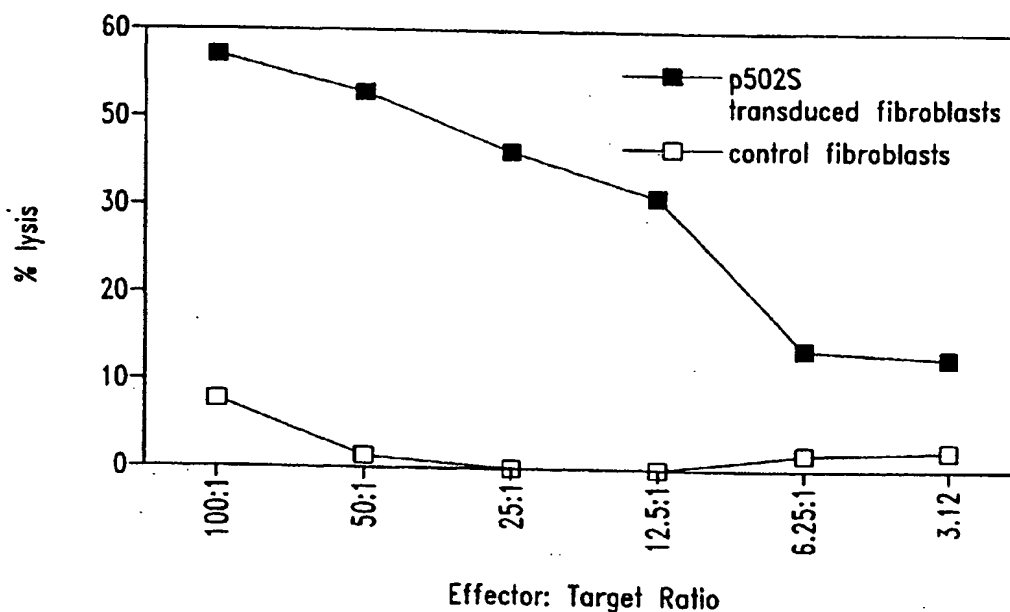
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(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly prostate cancer, are disclosed. Illustrative compositions comprise one or more prostate-specific polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly prostate cancer.

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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides, comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides are useful in pharmaceutical compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of prostate cancer.

10 BACKGROUND OF THE INVENTION

Cancer is a significant health problem throughout the world. Although Cancer is a significant health problem throughout the world. Although advances have been made in detection and therapy of cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of

prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other
5 cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide
10 compositions comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and
15 942;

(b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-
20 931, 938, 939 and 942;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;
25

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-

606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of prostate tissue samples tested, at a level that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for other normal tissues.

The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

The present invention further provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855,

858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943.

In certain preferred embodiments, the polypeptides and/or polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858 or 860-862, or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant, together with a physiologically acceptable carrier.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

5 Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

10 Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

 The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides
15 encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating and/or enhancing the expression,
20 purification and/or immunogenicity of the polypeptide(s).

 Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The patient may be afflicted with prostate cancer, in which case the methods provide
25 treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

 Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition as recited above. The patient may be afflicted

with prostate cancer, in which case the methods provide treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological
5 sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the polypeptide from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological
10 sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen presenting cell that
15 expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a
20 patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a
25 polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for
30 determining the presence or absence of a cancer, preferably a prostate cancer, in a

patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide of the present invention, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to an inventive polynucleotide, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample

obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate-specific polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/neu.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

5 Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

 Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell
10 line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

15 Figure 7 is a Western blot showing the expression of P501S in baculovirus.

 Figure 8 illustrates the results of epitope mapping studies on P501S.

 Figure 9 is a schematic representation of the P501S protein showing the
20 location of transmembrane domains and predicted intracellular and extracellular domains.

 Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of chromosome 22q11.2

25 Figure 11 shows the results of an ELISA assay to determine the specificity of rabbit polyclonal antisera raised against P501S.

 Figures 12A(1), 12A(2), 12A(3), and B are the full-length cDNA (SEQ ID NO:777) and predicted amino acid (SEQ ID NO:778) sequences, respectively, for the clone P788P.

 SEQ ID NO: 1 is the determined cDNA sequence for F1-13

30 SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12
SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16
SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1
SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9
5 SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4
SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12
10 SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862
SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19
15 SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19
SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24
20 SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58
SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58
SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4
25 SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4
SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16
30 SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21

SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48
SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6
5 SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858
SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861
SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864
SEQ ID NO: 41 is the determined cDNA sequence for P5
10 SEQ ID NO: 42 is the determined cDNA sequence for P8
SEQ ID NO: 43 is the determined cDNA sequence for P9
SEQ ID NO: 44 is the determined cDNA sequence for P18
SEQ ID NO: 45 is the determined cDNA sequence for P20
SEQ ID NO: 46 is the determined cDNA sequence for P29
15 SEQ ID NO: 47 is the determined cDNA sequence for P30
SEQ ID NO: 48 is the determined cDNA sequence for P34
SEQ ID NO: 49 is the determined cDNA sequence for P36
SEQ ID NO: 50 is the determined cDNA sequence for P38
SEQ ID NO: 51 is the determined cDNA sequence for P39
20 SEQ ID NO: 52 is the determined cDNA sequence for P42
SEQ ID NO: 53 is the determined cDNA sequence for P47
SEQ ID NO: 54 is the determined cDNA sequence for P49
SEQ ID NO: 55 is the determined cDNA sequence for P50
SEQ ID NO: 56 is the determined cDNA sequence for P53
25 SEQ ID NO: 57 is the determined cDNA sequence for P55
SEQ ID NO: 58 is the determined cDNA sequence for P60
SEQ ID NO: 59 is the determined cDNA sequence for P64
SEQ ID NO: 60 is the determined cDNA sequence for P65
SEQ ID NO: 61 is the determined cDNA sequence for P73
30 SEQ ID NO: 62 is the determined cDNA sequence for P75

SEQ ID NO: 63 is the determined cDNA sequence for P76

SEQ ID NO: 64 is the determined cDNA sequence for P79

SEQ ID NO: 65 is the determined cDNA sequence for P84

SEQ ID NO: 66 is the determined cDNA sequence for P68

5 SEQ ID NO: 67 is the determined cDNA sequence for P80 (also referred
to as P704P)

SEQ ID NO: 68 is the determined cDNA sequence for P82

SEQ ID NO: 69 is the determined cDNA sequence for U1-3064

SEQ ID NO: 70 is the determined cDNA sequence for U1-3065

10 SEQ ID NO: 71 is the determined cDNA sequence for V1-3692

SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905

SEQ ID NO: 73 is the determined cDNA sequence for V1-3686

SEQ ID NO: 74 is the determined cDNA sequence for R1-2330

SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976

15 SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736

SEQ ID NO: 78 is the determined cDNA sequence for 1G-4738

SEQ ID NO: 79 is the determined cDNA sequence for 1G-4741

SEQ ID NO: 80 is the determined cDNA sequence for 1G-4744

20 SEQ ID NO: 81 is the determined cDNA sequence for 1G-4734

SEQ ID NO: 82 is the determined cDNA sequence for 1H-4774

SEQ ID NO: 83 is the determined cDNA sequence for 1H-4781

SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785

SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787

25 SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796

SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807

SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810

SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811

SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876

30 SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884

SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896

SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761

SEQ ID NO: 94 is the determined cDNA sequence for 1G-4762

SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766

5 SEQ ID NO: 96 is the determined cDNA sequence for 1H-4770

SEQ ID NO: 97 is the determined cDNA sequence for 1H-4771

SEQ ID NO: 98 is the determined cDNA sequence for 1H-4772

SEQ ID NO: 99 is the determined cDNA sequence for 1D-4297

SEQ ID NO: 100 is the determined cDNA sequence for 1D-4309

10 SEQ ID NO: 101 is the determined cDNA sequence for 1D.1-4278

SEQ ID NO: 102 is the determined cDNA sequence for 1D-4288

SEQ ID NO: 103 is the determined cDNA sequence for 1D-4283

SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304

SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296

15 SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280

SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12

(also referred to as P504S)

SEQ ID NO: 108 is the predicted amino acid sequence for F1-12

SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17

20 SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12

(also referred to as P501S)

SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862 (also referred to as P503S)

SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

25 SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also referred to as P503S)

SEQ ID NO: 115 is the determined cDNA sequence for P89

30 SEQ ID NO: 116 is the determined cDNA sequence for P90

SEQ ID NO: 117 is the determined cDNA sequence for P92
SEQ ID NO: 118 is the determined cDNA sequence for P95
SEQ ID NO: 119 is the determined cDNA sequence for P98
SEQ ID NO: 120 is the determined cDNA sequence for P102
5 SEQ ID NO: 121 is the determined cDNA sequence for P110
SEQ ID NO: 122 is the determined cDNA sequence for P111
SEQ ID NO: 123 is the determined cDNA sequence for P114
SEQ ID NO: 124 is the determined cDNA sequence for P115
SEQ ID NO: 125 is the determined cDNA sequence for P116
10 SEQ ID NO: 126 is the determined cDNA sequence for P124
SEQ ID NO: 127 is the determined cDNA sequence for P126
SEQ ID NO: 128 is the determined cDNA sequence for P130
SEQ ID NO: 129 is the determined cDNA sequence for P133
SEQ ID NO: 130 is the determined cDNA sequence for P138
15 SEQ ID NO: 131 is the determined cDNA sequence for P143
SEQ ID NO: 132 is the determined cDNA sequence for P151
SEQ ID NO: 133 is the determined cDNA sequence for P156
SEQ ID NO: 134 is the determined cDNA sequence for P157
SEQ ID NO: 135 is the determined cDNA sequence for P166
20 SEQ ID NO: 136 is the determined cDNA sequence for P176
SEQ ID NO: 137 is the determined cDNA sequence for P178
SEQ ID NO: 138 is the determined cDNA sequence for P179
SEQ ID NO: 139 is the determined cDNA sequence for P185
SEQ ID NO: 140 is the determined cDNA sequence for P192
25 SEQ ID NO: 141 is the determined cDNA sequence for P201
SEQ ID NO: 142 is the determined cDNA sequence for P204
SEQ ID NO: 143 is the determined cDNA sequence for P208
SEQ ID NO: 144 is the determined cDNA sequence for P211
SEQ ID NO: 145 is the determined cDNA sequence for P213
30 SEQ ID NO: 146 is the determined cDNA sequence for P219

SEQ ID NO: 147 is the determined cDNA sequence for P237

SEQ ID NO: 148 is the determined cDNA sequence for P239

SEQ ID NO: 149 is the determined cDNA sequence for P248

SEQ ID NO: 150 is the determined cDNA sequence for P251

5 SEQ ID NO: 151 is the determined cDNA sequence for P255

SEQ ID NO: 152 is the determined cDNA sequence for P256

SEQ ID NO: 153 is the determined cDNA sequence for P259

SEQ ID NO: 154 is the determined cDNA sequence for P260

SEQ ID NO: 155 is the determined cDNA sequence for P263

10 SEQ ID NO: 156 is the determined cDNA sequence for P264

SEQ ID NO: 157 is the determined cDNA sequence for P266

SEQ ID NO: 158 is the determined cDNA sequence for P270

SEQ ID NO: 159 is the determined cDNA sequence for P272

SEQ ID NO: 160 is the determined cDNA sequence for P278

15 SEQ ID NO: 161 is the determined cDNA sequence for P105

SEQ ID NO: 162 is the determined cDNA sequence for P107

SEQ ID NO: 163 is the determined cDNA sequence for P137

SEQ ID NO: 164 is the determined cDNA sequence for P194

SEQ ID NO: 165 is the determined cDNA sequence for P195

20 SEQ ID NO: 166 is the determined cDNA sequence for P196

SEQ ID NO: 167 is the determined cDNA sequence for P220

SEQ ID NO: 168 is the determined cDNA sequence for P234

SEQ ID NO: 169 is the determined cDNA sequence for P235

SEQ ID NO: 170 is the determined cDNA sequence for P243

25 SEQ ID NO: 171 is the determined cDNA sequence for P703P-DE1

SEQ ID NO: 172 is the predicted amino acid sequence for P703P-DE1

SEQ ID NO: 173 is the determined cDNA sequence for P703P-DE2

SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6

SEQ ID NO: 175 is the determined cDNA sequence for P703P-DE13

30 SEQ ID NO: 176 is the predicted amino acid sequence for P703P-DE13

SEQ ID NO: 177 is the determined cDNA sequence for P703P-DE14

SEQ ID NO: 178 is the predicted amino acid sequence for P703P-DE14

SEQ ID NO: 179 is the determined extended cDNA sequence for 1G-

4736

5 SEQ ID NO: 180 is the determined extended cDNA sequence for 1G-

4738

SEQ ID NO: 181 is the determined extended cDNA sequence for 1G-

4741

SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-

10 4744

SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-

4774

SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-

4781

15 SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-

4785

SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-

4787

SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-

20 4796

SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-

4807

SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810

SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811

25 SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-

4876

SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-

4884

SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-

30 4896

- 4761 SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-
- 4762 SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-
- 5 4766 SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-
- SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770
- SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771
- 10 4772 SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-
- SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-
- 4309 SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-
- 4278 SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-
- 15 4288 SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-
- 4283 SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-
- 20 4304 SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-
- 4296 SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-
- 4280 SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
- 25 SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
- SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
- SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
- SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
- 30 SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd

SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
5 SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev
SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
10 SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
SEQ ID NO: 223 is the determined cDNA sequence for P509S
SEQ ID NO: 224 is the determined cDNA sequence for P510S
SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
15 SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13
SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23
20 SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25
SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35
25 SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38
SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41
30 SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42

SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56
5 SEQ ID NO: 247 is the determined cDNA sequence for PTPN64
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
10 SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
15 SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2
SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3
20 SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
25 SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
30 SEQ ID NO: 272 is the determined cDNA sequence for JP1A9

SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
5 SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
10 SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
15 SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
20 SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
25 SEQ ID NO: 297 is the determined cDNA sequence for JP8B10
SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
30 SEQ ID NO: 302 is the determined cDNA sequence for JP8H9

SEQ ID NO: 303 is the determined cDNA sequence for JP8C12

SEQ ID NO: 304 is the determined cDNA sequence for JP8E11

SEQ ID NO: 305 is the determined cDNA sequence for JP8E12

SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12

5 SEQ ID NO: 307 is the determined cDNA sequence for P711P

SEQ ID NO: 308 is the determined cDNA sequence for P712P

SEQ ID NO: 309 is the determined cDNA sequence for CLONE23

SEQ ID NO: 310 is the determined cDNA sequence for P774P

SEQ ID NO: 311 is the determined cDNA sequence for P775P

10 SEQ ID NO: 312 is the determined cDNA sequence for P715P

SEQ ID NO: 313 is the determined cDNA sequence for P710P

SEQ ID NO: 314 is the determined cDNA sequence for P767P

SEQ ID NO: 315 is the determined cDNA sequence for P768P

15 isolated genes
SEQ ID NO: 316-325 are the determined cDNA sequences of previously

SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5

SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5

SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26

SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26

20 SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23

SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23

SEQ ID NO: 332 is the determined full length cDNA sequence for

P509S

25 SEQ ID NO: 333 is the determined extended cDNA sequence for P707P
(also referred to as 11-C9)

SEQ ID NO: 334 is the determined cDNA sequence for P714P

SEQ ID NO: 335 is the determined cDNA sequence for P705P (also
referred to as 9-F3)

SEQ ID NO: 336 is the predicted amino acid sequence for P705P

30 SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

SEQ ID NO: 338 is the amino acid sequence of the peptide p5

SEQ ID NO: 339 is the predicted amino acid sequence of P509S

SEQ ID NO: 340 is the determined cDNA sequence for P778P

SEQ ID NO: 341 is the determined cDNA sequence for P786P

5 SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing
homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing
homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

10 SEQ ID NO: 345 is the determined cDNA sequence for a clone showing
homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing
homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase
(SHMT)

15 SEQ ID NO: 347 is the determined cDNA sequence for a clone showing
homology to Homo sapiens natural resistance-associated macrophage protein2
(NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing
homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

20 SEQ ID NO: 349 is the determined cDNA sequence for a clone showing
homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

25 SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

30 SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

5 SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

10 SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

15 SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

20 SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

25 SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO: 386 is the cDNA sequence for 23320.

SEQ ID NO: 387 is the cDNA sequence for CGI-69.

SEQ ID NO: 388 is the cDNA sequence for L-iditol-2-dehydrogenase.

SEQ ID NO: 389 is the cDNA sequence for 23379.

30 SEQ ID NO: 390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

5 SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor

PDEF.

10 SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

15 SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553 (also known as

P1020C).

20 SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

25 SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.

SEQ ID NO:415 is the cDNA sequence for 22572.

SEQ ID NO:416 is the cDNA sequence for 22573.

SEQ ID NO:417 is the cDNA sequence for 22573.

30 SEQ ID NO:418 is the cDNA sequence for 22575.

SEQ ID NO:419 is the cDNA sequence for 22580.

SEQ ID NO:420 is the cDNA sequence for 22581.

SEQ ID NO:421 is the cDNA sequence for 22582.

SEQ ID NO:422 is the cDNA sequence for 22583.

5 SEQ ID NO:423 is the cDNA sequence for 22584.

SEQ ID NO:424 is the cDNA sequence for 22585.

SEQ ID NO:425 is the cDNA sequence for 22586.

SEQ ID NO:426 is the cDNA sequence for 22587.

SEQ ID NO:427 is the cDNA sequence for 22588.

10 SEQ ID NO:428 is the cDNA sequence for 22589.

SEQ ID NO:429 is the cDNA sequence for 22590.

SEQ ID NO:430 is the cDNA sequence for 22591.

SEQ ID NO:431 is the cDNA sequence for 22592.

SEQ ID NO:432 is the cDNA sequence for 22593.

15 SEQ ID NO:433 is the cDNA sequence for 22594.

SEQ ID NO:434 is the cDNA sequence for 22595.

SEQ ID NO:435 is the cDNA sequence for 22596.

SEQ ID NO:436 is the cDNA sequence for 22847.

SEQ ID NO:437 is the cDNA sequence for 22848.

20 SEQ ID NO:438 is the cDNA sequence for 22849.

SEQ ID NO:439 is the cDNA sequence for 22851.

SEQ ID NO:440 is the cDNA sequence for 22852.

SEQ ID NO:441 is the cDNA sequence for 22853.

SEQ ID NO:442 is the cDNA sequence for 22854.

25 SEQ ID NO:443 is the cDNA sequence for 22855.

SEQ ID NO:444 is the cDNA sequence for 22856.

SEQ ID NO:445 is the cDNA sequence for 22857.

SEQ ID NO:446 is the cDNA sequence for 23601.

SEQ ID NO:447 is the cDNA sequence for 23602.

30 SEQ ID NO:448 is the cDNA sequence for 23605.

SEQ ID NO:449 is the cDNA sequence for 23606.

SEQ ID NO:450 is the cDNA sequence for 23612.

SEQ ID NO:451 is the cDNA sequence for 23614.

SEQ ID NO:452 is the cDNA sequence for 23618.

5 SEQ ID NO:453 is the cDNA sequence for 23622.

SEQ ID NO:454 is the cDNA sequence for folate hydrolase.

SEQ ID NO:455 is the cDNA sequence for LIM protein.

SEQ ID NO:456 is the cDNA sequence for a known gene.

SEQ ID NO:457 is the cDNA sequence for a known gene.

10 SEQ ID NO:458 is the cDNA sequence for a previously identified gene.

SEQ ID NO:459 is the cDNA sequence for 23045.

SEQ ID NO:460 is the cDNA sequence for 23032.

SEQ ID NO:461 is the cDNA sequence for clone 23054.

SEQ ID NO:462-467 are cDNA sequences for known genes.

15 SEQ ID NO:468-471 are cDNA sequences for P710P.

SEQ ID NO:472 is a cDNA sequence for P1001C.

SEQ ID NO: 473 is the determined cDNA sequence for a first splice variant of P775P (referred to as 27505).

20 SEQ ID NO: 474 is the determined cDNA sequence for a second splice variant of P775P (referred to as 19947).

SEQ ID NO: 475 is the determined cDNA sequence for a third splice variant of P775P (referred to as 19941).

SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice variant of P775P (referred to as 19937).

25 SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

SEQ ID NO: 478 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

30 SEQ ID NO: 479 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 475.

SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

5. SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

10. SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 485 is the PCR primer AW025.

SEQ ID NO: 486 is the PCR primer AW003.

SEQ ID NO: 487 is the PCR primer AW027.

SEQ ID NO: 488 is the PCR primer AW026.

15. SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.

SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.

SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.

20. SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.

SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.

25. SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.

SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.

SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.

30. SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P.

SEQ ID NO: 524 is the putative full-length cDNA sequence of P703P.

SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ ID NO: 524.

SEQ ID NO: 526 is the full-length cDNA sequence for P790P.

5 SEQ ID NO: 527 is the predicted amino acid sequence for P790P.

SEQ ID NO: 528 & 529 are PCR primers.

SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID NO: 366.

10 SEQ ID NO: 531 is the cDNA sequence of the open reading frame of SEQ ID NO: 530.

SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of SEQ ID NO: 531.

SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.

15 SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ ID NO: 533.

SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.

SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.

SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ ID NO: 535.

20 SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ ID NO: 536.

SEQ ID NO: 539 is the peptide P501S-370.

SEQ ID NO: 540 is the peptide P501S-376.

SEQ ID NO: 541-551 are epitopes of P501S.

25 SEQ ID NO: 552 is an extended cDNA sequence for P712P.

SEQ ID NO: 553-568 are the amino acid sequences encoded by predicted open reading frames within SEQ ID NO: 552.

SEQ ID NO: 569 is an extended cDNA sequence for P776P.

30 SEQ ID NO: 570 is the determined cDNA sequence for a splice variant of P776P referred to as contig 6.

SEQ ID NO: 571 is the determined cDNA sequence for a splice variant of P776P referred to as contig 7.

SEQ ID NO: 572 is the determined cDNA sequence for a splice variant of P776P referred to as contig 14.

5 SEQ ID NO: 573 is the amino acid sequence encoded by a first predicted ORF of SEQ ID NO: 570.

SEQ ID NO: 574 is the amino acid sequence encoded by a second predicted ORF of SEQ ID NO: 570.

10 SEQ ID NO: 575 is the amino acid sequence encoded by a predicted ORF of SEQ ID NO: 571.

SEQ ID NO: 576-586 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 569.

SEQ ID NO: 587 is a DNA consensus sequence of the sequences of P767P and P777P.

15 SEQ ID NO: 588-590 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 587.

SEQ ID NO: 591 is an extended cDNA sequence for P1020C.

SEQ ID NO: 592 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: P1020C.

20 SEQ ID NO: 593 is a splice variant of P775P referred to as 50748.

SEQ ID NO: 594 is a splice variant of P775P referred to as 50717. SEQ ID NO: 595 is a splice variant of P775P referred to as 45985.

SEQ ID NO: 596 is a splice variant of P775P referred to as 38769.

SEQ ID NO: 597 is a splice variant of P775P referred to as 37922.

25 SEQ ID NO: 598 is a splice variant of P510S referred to as 49274.

SEQ ID NO: 599 is a splice variant of P510S referred to as 39487.

SEQ ID NO: 600 is a splice variant of P504S referred to as 5167.16.

SEQ ID NO: 601 is a splice variant of P504S referred to as 5167.1.

SEQ ID NO: 602 is a splice variant of P504S referred to as 5163.46.

30 SEQ ID NO: 603 is a splice variant of P504S referred to as 5163.42.

SEQ ID NO: 604 is a splice variant of P504S referred to as 5163.34.

SEQ ID NO: 605 is a splice variant of P504S referred to as 5163.17.

SEQ ID NO: 606 is a splice variant of P501S referred to as 10640.

SEQ ID NO: 607-615 are the sequences of PCR primers.

5 SEQ ID NO: 616 is the determined cDNA sequence of a fusion of P703P
and PSA.

SEQ ID NO: 617 is the amino acid sequence of the fusion of P703P and
PSA.

10 SEQ ID NO: 618-689 are determined cDNA sequences of prostate-
specific clones.

SEQ ID NO: 690 is the cDNA sequence of the gene DD3.

SEQ ID NO: 691-697 are determined cDNA sequences of prostate-
specific clones.

SEQ ID NO: 698 is an extended cDNA sequence for P714P.

15 SEQ ID NO: 699-701 are the cDNA sequences for splice variants of
P704P.

SEQ ID NO: 702 is the cDNA sequence of a spliced variant of P553S
referred to as P553S-14.

20 SEQ ID NO: 703 is the cDNA sequence of a spliced variant of P553S
referred to as P553S-12.

SEQ ID NO: 704 is the cDNA sequence of a spliced variant of P553S
referred to as P553S-10.

SEQ ID NO: 705 is the cDNA sequence of a spliced variant of P553S
referred to as P553S-6.

25 SEQ ID NO: 706 is the amino acid sequence encoded by SEQ ID NO:
705.

SEQ ID NO: 707 is the amino acid sequence encoded by SEQ ID NO:
702 SEQ ID NO: 708 is a second amino acid sequence encoded by SEQ ID NO: 702.

30 SEQ ID NO: 709-772 are determined cDNA sequences of prostate-
specific clones.

SEQ ID NO: 773 is a first full-length cDNA sequence for prostate-specific transglutaminase gene (also referred to herein as P558S).

SEQ ID NO: 774 is a second full-length cDNA sequence for prostate-specific transglutaminase gene.

5. SEQ ID NO: 775 is the amino acid sequence encoded by the sequence of SEQ ID NO: 773.

SEQ ID NO: 776 is the amino acid sequence encoded by the sequence of SEQ ID NO: 774.

SEQ ID NO: 777 is the full-length cDNA sequence for P788P.

10 SEQ ID NO: 778 is the amino acid sequence encoded by SEQ ID NO: 777.

SEQ ID NO: 779 is the determined cDNA sequence for a polymorphic variant of P788P.

15 SEQ ID NO: 780 is the amino acid sequence encoded by SEQ ID NO: 779.

SEQ ID NO: 781 is the amino acid sequence of peptide 4 from P703P.

SEQ ID NO: 782 is the cDNA sequence that encodes peptide 4 from P703P.

20 SEQ ID NO: 783-798 are the cDNA sequence encoding epitopes of P703P.

SEQ ID NO: 799-814 are the amino acid sequences of epitopes of P703P.

SEQ ID NO: 815 and 816 are PCR primers.

25 SEQ ID NO: 817 is the cDNA sequence encoding an N-terminal portion of P788P expressed in *E. coli*.

SEQ ID NO: 818 is the amino acid sequence of the N-terminal portion of P788P expressed in *E. coli*.

SEQ ID NO: 819 is the amino acid sequence of the *M. tuberculosis* antigen Ra12.

30 SEQ ID NO: 820 and 821 are PCR primers.

SEQ ID NO: 822 is the cDNA sequence for the Ra12-P510S-C construct.

SEQ ID NO: 823 is the cDNA sequence for the P510S-C construct.

SEQ ID NO: 824 is the cDNA sequence for the P510S-E3 construct.

5 SEQ ID NO: 825 is the amino acid sequence for the Ra12-P510S-C construct.

SEQ ID NO: 826 is the amino acid sequence for the P510S-C construct.

SEQ ID NO: 827 is the amino acid sequence for the P510S-E3 construct.

SEQ ID NO: 828-833 are PCR primers.

10 SEQ ID NO: 834 is the cDNA sequence of the construct Ra12-P775P-ORF3.

SEQ ID NO: 835 is the amino acid sequence of the construct Ra12-P775P-ORF3.

SEQ ID NO: 836 and 837 are PCR primers.

15 SEQ ID NO: 838 is the determined amino acid sequence for a P703P His tag fusion protein.

SEQ ID NO: 839 is the determined cDNA sequence for a P703P His tag fusion protein.

SEQ ID NO: 840 and 841 are PCR primers.

20 SEQ ID NO: 842 is the determined amino acid sequence for a P705P His tag fusion protein.

SEQ ID NO: 843 is the determined cDNA sequence for a P705P His tag fusion protein.

SEQ ID NO: 844 and 845 are PCR primers.

25 SEQ ID NO: 846 is the determined amino acid sequence for a P711P His tag fusion protein.

SEQ ID NO: 847 is the determined cDNA sequence for a P711P His tag fusion protein.

30 SEQ ID NO: 848 is the amino acid sequence of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 849 and 850 are PCR primers.

SEQ ID NO: 851 is the determined cDNA sequence for the construct Ra12-P501S-E2.

5 SEQ ID NO: 852 is the determined amino acid sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 853 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 854 is the DNA sequence encoding SEQ ID NO: 853.

SEQ ID NO: 855 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 856 is the DNA sequence encoding SEQ ID NO: 855.

10 SEQ ID NO: 857 is a peptide employed in epitope mapping studies.

SEQ ID NO: 858 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 859 is the DNA sequence encoding SEQ ID NO: 858.

SEQ ID NO: 860-862 are the amino acid sequences for CD4 epitopes of P501S.

15 SEQ ID NO: 863-865 are the DNA sequences encoding the sequences of SEQ ID NO: 860-862.

SEQ ID NO: 866-877 are the amino acid sequences for putative CTL epitopes of P703P.

SEQ ID NO: 878 is the full-length cDNA sequence for P789P.

20 SEQ ID NO: 879 is the amino acid sequence encoded by SEQ ID NO: 878.

SEQ ID NO: 880 is the determined full-length cDNA sequence for the splice variant of P776P referred to as contig 6.

25 SEQ ID NO: 881-882 are determined full-length cDNA sequences for the splice variant of P776P referred to as contig 7.

SEQ ID NO: 883-887 are amino acid sequences encoded by SEQ ID NO: 880.

SEQ ID NO: 888-893 are amino acid sequences encoded by the splice variant of P776P referred to as contig 7.

SEQ ID NO: 894 is the full-length cDNA sequence for human transmembrane protease serine 2.

SEQ ID NO: 895 is the amino acid sequence encoded by SEQ ID NO: 894.

5 SEQ ID NO: 896 is the cDNA sequence encoding the first 209 amino acids of human transmembrane protease serine 2.

SEQ ID NO: 897 is the first 209 amino acids of human transmembrane protease serine 2.

10 SEQ ID NO: 898 is the amino acid sequence of peptide 296-322 of P501S.

SEQ ID NO: 899-902 are PCR primers.

SEQ ID NO: 903 is the determined cDNA sequence of the Vb chain of a T cell receptor for the P501S-specific T cell clone 4E5.

15 SEQ ID NO: 904 is the determined cDNA sequence of the Va chain of a T cell receptor for the P501S-specific T cell clone 4E5.

SEQ ID NO: 905 is the amino acid sequence encoded by SEQ ID NO 903.

SEQ ID NO: 906 is the amino acid sequence encoded by SEQ ID NO 904.

20 SEQ ID NO: 907 is the full-length open reading frame for P768P including stop codon.

SEQ ID NO: 908 is the full-length open reading frame for P768P without stop codon.

25 SEQ ID NO: 909 is the amino acid sequence encoded by SEQ ID NO: 908.

SEQ ID NO: 910-915 are the amino acid sequences for predicted domains of P768P.

SEQ ID NO: 916 is the full-length cDNA sequence of P835P.

30 SEQ ID NO: 917 is the cDNA sequence of the previously identified clone FLJ13581.

SEQ ID NO: 918 is the cDNA sequence of the open reading frame for P835P with stop codon.

SEQ ID NO: 919 is the cDNA sequence of the open reading frame for P835P without stop codon.

5 SEQ ID NO: 920 is the full-length amino acid sequence for P835P.

SEQ ID NO: 921-928 are the amino acid sequences of extracellular and intracellular domains of P835P.

SEQ ID NO: 929 is the full-length cDNA sequence for P1000C.

10 SEQ ID NO: 930 is the cDNA sequence of the open reading frame for P1000C, including stop codon.

SEQ ID NO: 931 is the cDNA sequence of the open reading frame for P1000C, without stop codon.

SEQ ID NO: 932 is the full-length amino acid sequence for P1000C.

SEQ ID NO: 933 is amino acids 1-100 of SEQ ID NO: 932.

15 SEQ ID NO: 934 is amino acids 100-492 of SEQ ID NO: 932.

SEQ ID NO: 935-937 are PCR primers.

SEQ ID NO: 938 is the cDNA sequence of the expressed full-length P767P coding region.

20 SEQ ID NO: 939 is the cDNA sequence of an expressed truncated P767P coding region.

SEQ ID NO: 940 is the amino acid sequence encoded by SEQ ID NO: 939.

SEQ ID NO: 941 is the amino acid sequence encoded by SEQ ID NO: 938.

25 SEQ ID NO: 942 is the DNA sequence of a CD4 epitope of P703P.

SEQ ID NO: 943 is the amino acid sequence of a CD4 epitope of P703P.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly prostate cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (e.g., T cells).

The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, e.g., Sambrook, et al. Molecular Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis et al. Molecular Cloning: A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether supra or infra, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

Polypeptide Compositions

As used herein, the term "polypeptide" is used in its conventional meaning, i.e., as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-

expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942. In specific embodiments, the polypeptides of the invention comprise amino acid sequences as set forth in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943.

The polypeptides of the present invention are sometimes herein referred to as prostate-specific proteins or prostate-specific polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in prostate tissue samples. Thus, a "prostate-specific polypeptide" or "prostate-specific protein," refers generally to a polypeptide sequence of the present invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed

in a substantial proportion of prostate tissue samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of prostate tissue samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in other
5 normal tissues, as determined using a representative assay provided herein. A prostate-specific polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

In certain preferred embodiments, the polypeptides of the invention are
10 immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with prostate cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory*
15 *Manual*, Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

20 As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.*, specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide.
25 Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they
30 specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other

immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain has been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide composition set forth herein, such as those set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-
5 380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-
10 335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally
15 encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%; or 99% or more identity (determined as described below), along its length, to a polypeptide sequence set forth herein.

In one preferred embodiment, the polypeptide fragments and variants
20 provided by the present invention are immunologically reactive with an antibody and/or T-cell that reacts with a full-length polypeptide specifically set forth herein.

In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or
25 more of that exhibited by a full-length polypeptide sequence specifically set forth herein.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally
30 occurring or may be synthetically generated, for example, by modifying one or more of

the above polypeptide sequences of the invention and evaluating their immunogenic activity as described herein using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader
5 sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another
10 amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide
15 with desirable characteristics, *e.g.*, with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

For example, certain amino acids may be substituted for other amino
20 acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence
25 substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.
30

TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its

hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5);
5 glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are
10 within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of
15 its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 \pm 1); glutamate (+3.0 \pm 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5 \pm 1); alanine (−0.5); histidine (−0.5); cysteine
20 (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−2.3); phenylalanine (−2.5); tryptophan (−3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2
25 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that
30 take various of the foregoing characteristics into consideration are well known to those

of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of
5 flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

10 Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values
15 include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a
20 preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

25 As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For
30 example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

- Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

- Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics

Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known

tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al.,

Proc. Natl. Acad. Sci. USA 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to
5 separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and
10 transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus,
15 tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

In one preferred embodiment, the immunological fusion partner is derived from a *Mycobacterium* sp., such as a *Mycobacterium tuberculosis*-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression
20 and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent
25 and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; *see also, Skeiky et al., Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the
30 purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous

immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine

amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been
5 exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at
10 residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention,
15 when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of CD4⁺ T-cells specific for the polypeptide.

Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further
20 described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a
25 growing amino acid chain. *See Merrifield, J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of
30 the invention are isolated. An "isolated" polypeptide is one that is removed from its

original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably an immunogenic variant or derivative, of such a sequence.

5 Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823,
10 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, complements of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-
15 931, 938, 939 and 942, and degenerate variants of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942. In certain preferred
20 embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

 In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-
25 335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide sequence of this
30 invention using the methods described herein, (*e.g.*, BLAST analysis using standard

parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

5 Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth herein). The term "variants" should also be understood to encompass homologous
10 genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to, or complementary to, one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at
15 least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103,
20 *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary
25 sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for
30 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in

the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the
5 exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides that are immunologically cross-reactive with a polypeptide sequence specifically set
10 forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

The polynucleotides of the present invention, or fragments thereof,
15 regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by
20 the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

25 When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison
30 window" as used herein, refers to a segment of at least about 20 contiguous positions,

usually 30 to about 75, preferably 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent

sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present

invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25

nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single
5 stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

10 In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded
15 vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected
20 which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be
25 obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable
5 signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known
10 rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

15 In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

20 In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 contiguous nucleotides that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence
25 disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, e.g., those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a
30 sequence of interest will enable them to be of use in detecting the presence of

complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of
5 contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in
10 various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger
15 contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in
20 length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

25 Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various

factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, e.g., one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to

destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention, 5 polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis 10 is well established. For example, the synthesis of polygalacturonase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, 15 striatal GABA_A receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a 20 variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a 25 complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In 30 each case, preferred compositions comprise a sequence region that is complementary,

and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m , binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.*, Nucleic Acids Res. 1997 Sep 1;25(17):3389-402).

The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a

high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement
5 that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general,
10 enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to
15 cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many
20 technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of
25 target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action
30 (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the

specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* Nucleic Acids Res. 1992 Sep 11;20(17):4559-65. Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz, Biochemistry 1989 Jun 13;28(12):4929-33; Hampel *et al.*, Nucleic Acids Res. 1990 Jan 25;18(2):299-304 and U. S. Patent 5,631,359. An example of the hepatitis δ virus motif is described by Perrotta and Been, Biochemistry. 1992 Dec 1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive, Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO

92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells. Ribozymes

expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, *Antisense Nucleic Acid Drug Dev.* 1997 7(4) 431-37). PNA is able to be utilized in a number of methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, *Science*. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, *Bioorg Med Chem.* 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*,

Bioorg Med Chem. 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will
5 depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed
10 by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that
15 contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and
20 utilized modifications of PNAs (for example, Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45; Petersen *et al.*, J Pept Sci. 1995 May-Jun;1(3):175-83; Orum *et al.*, Biotechniques. 1995 Sep;19(3):472-80; Footer *et al.*, Biochemistry. 1996 Aug 20;35(33):10673-9; Griffith *et al.*, Nucleic Acids Res. 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, Proc Natl Acad Sci U S A. 1995 Jun 6;92(12):5592-6; Boffa *et al.*,
25 Proc Natl Acad Sci U S A. 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, Blood. 1996 Aug 15;88(4):1411-7; Armitage *et al.*, Proc Natl Acad Sci U S A. 1997 Nov 11;94(23):12320-5; Seeger *et al.*, Biotechniques. 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to
30 therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (Anal Chem. 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (Biochemistry. 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

Polynucleotide Identification, Characterization and Expression

Polynucleotide compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by

reference in its entirety. Briefly, in PCRTM, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present
5 in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse
10 transcription and PCRTM amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCRTM amplification technique, are readily known and available in
15 the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat.
20 Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded
25 RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara,
30 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (e.g., a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification.

5. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then be assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of

amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or
5 RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic. 1*:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res. 19*:3055-60, 1991). Other methods employing amplification may also be employed
10 to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs
15 may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct
20 expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous
25 in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring
30 sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

10 In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be
15 engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. 20 (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be
25 achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable
30 techniques available in the art. The composition of the synthetic peptides may be

confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

5 In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing
10 sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York.
15 N.Y.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid,
20 or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

25 The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription
30 and translation elements, including constitutive and inducible promoters, may be used.

For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For

example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which

successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or apt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of

skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

5 A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal
10 antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; *Serological Methods, a Laboratory Manual*, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

15 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions
20 thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used
25 include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

 Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained
30 intracellularly depending on the sequence and/or the vector used. As will be understood

by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

Antibody Compositions, Fragments Thereof and Other Binding Agents

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunologically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant K_d . See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as

"framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation

of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "F(ab)₂" fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V_H::V_L heterodimer including an antigen-binding site which retains much of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked V_H::V_L heterodimer which is expressed from a gene fusion including V_H- and V_L-encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated--but chemically separated--light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an

antigen-binding site. See, *e.g.*, U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRs and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (*e.g.*, a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRs. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures--regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) *Nature* 349:293-299; Lobuglio et al. (1989) *Proc. Nat. Acad. Sci. USA* 86:4220-4224; Shaw et al. (1987) *J Immunol.* 138:4534-4538; and Brown et al. (1987) *Cancer Res.* 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) *Nature* 332:323-327; Verhoeyen et al. (1988) *Science* 239:1534-1536; and Jones et al. (1986) *Nature* 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) *Ann. Rev. Biochem.* 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (*e.g.*, solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (*e.g.*, electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in

this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred
5 toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a
10 substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an
15 antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which
20 otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups,
25 sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of
30 different cleavable linker groups have been described. The mechanisms for the

intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by
5 serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody.
10 Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent
15 bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for
20 radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For
25 example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells

may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et

al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as

described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and therapeutic vaccine applications. Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, e.g., vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve

the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (e.g., U.S. Pat. No. 5,219,740; Miller and Rosman (1989) *BioTechniques* 7:980-990; Miller, A. D. (1990) *Human Gene Therapy* 1:5-14; Scarpa et al. (1991) *Virology* 180:849-852; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033-8037; and Boris-Lawrie and Temin (1993) *Cur. Opin. Genet. Develop.* 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) *J. Virol.* 57:267-274; Bett et al. (1993) *J. Virol.* 67:5911-5921; Mittereder et al. (1994) *Human Gene Therapy* 5:717-729; Seth et al. (1994) *J. Virol.* 68:933-940; Barr et al. (1994) *Gene Therapy* 1:51-58; Berkner, K. L. (1988) *BioTechniques* 6:616-629; and Rich et al. (1993) *Human Gene Therapy* 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, e.g., U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) *Molec. Cell. Biol.* 8:3988-3996; Vincent et al. (1990) *Vaccines 90* (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) *Current Opinion in Biotechnology* 3:533-539; Muzyczka, N. (1992) *Current Topics in Microbiol. and Immunol.* 158:97-129;

Kotin, R. M. (1994) Human Gene Therapy 5:793-801; Shelling and Smith (1994) Gene Therapy 1:165-169; and Zhou et al. (1994) J. Exp. Med. 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK^{sup}(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, e.g., Elroy-Stein and Moss, Proc. Natl. Acad. Sci. USA (1990) 87:6743-6747; Fuerst et al. Proc. Natl. Acad. Sci. USA (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer

protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant
5 Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, *e.g.*, WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in
10 U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et
15 al. *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103; 1989; Flexner
20 et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al.,
25 *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in a specific location and orientation
via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the
30 polynucleotide may be stably maintained in the cell as a separate, episomal segment of

DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression
5 construct employed.

In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable
10 beads, which are efficiently transported into the cells.

In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK)
15 and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device,
20 propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639
25 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances
30 or potentiates an immune response (antibody and/or cell-mediated) to an exogenous

antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins.

5 Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated
10 sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition
15 is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as
20 provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman,
25 *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL[®] adjuvants are available from Corixa Corporation (Seattle, WA; *see*, for example, US
30 Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing

oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by

5 Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins. Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example

10 combinations of at least two of the following group comprising QS21, QS7, Quil A, β -escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix,

15 particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or

20 suspension, or in a particulate structure such as a paucilamellar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol^R to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the

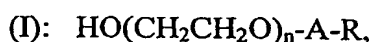
25 combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL[®] adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-

MPL[®] adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of
5 CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series
10 of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Enhanzyn[®]; Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene
15 ether adjuvants such as those described in WO 99/52549A1.

Other preferred adjuvants include adjuvant molecules of the general formula



wherein, n is 1-50, A is a bond or $-\text{C}(\text{O})-$, R is C_{1-50} alkyl or Phenyl C_{1-50} alkyl.

20 One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I), wherein n is between 1 and 50, preferably 4-24, most preferably 9; the R component is C_{1-50} , preferably $\text{C}_4\text{-C}_{20}$ alkyl and most preferably C_{12} alkyl, and A is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably
25 from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck
30 index (12th edition: entry 7717). These adjuvant molecules are described in WO

99/52549. The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

5 According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or
10 maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

15 Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In
20 general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex*
25 *vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

 Dendritic cells and progenitors may be obtained from peripheral blood,
30 bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph

nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from
5 peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature"
10 cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature
15 phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the
20 invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be
25 administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or
30 progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or

RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763;

5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems, such as described in WO/99 40934, and references cited therein, will also be useful for many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

The pharmaceutical compositions of the invention will often further comprise one or more buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they

may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia, cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

For oral administration, the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or

by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride.

- 5 Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered
10 isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml
15 of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity
20 standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for
25 example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be

administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption
5 delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase
10 "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the
15 lungs *via* nasal aerosol sprays has been described, *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of
20 a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid
25 particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example,
30 Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998

Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

5 Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery
10 systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, the use of liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

15 In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)).

 Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the
20 present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μ m) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for
25 example, by Couvreur *et al.*, Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

Cancer Therapeutic Methods

In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of prostate cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The

polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous,

intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 μ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies)

obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the
5 biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in
10 the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c)
15 comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding
20 agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized
25 binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and polypeptide portions thereof to which the binding agent binds, as
30 described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized

on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a
5 different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically
10 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact
15 time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve
20 equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second
25 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of
30 binding that occurs over a period of time. Unbound detection reagent is then removed

and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10

nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the
5 diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold*
10 *Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules.
15 PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold
20 or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above
25 for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the

cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound
5 binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific
10 for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

15 The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein.
20 Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

25 Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be

present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

5

EXAMPLES

EXAMPLE 1

5 ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from
10 prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA
15 was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns
20 (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA
25 libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones
30 having inserts and the average insert size being 1120 base pairs. For both libraries,

sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor
5 and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol
10 precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the
15 DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of
20 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three
25 more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E.*

coli DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12 (also referred to as P504S). This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108. cDNA splice variants of P504S are provided in SEQ ID NO: 600-605.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and

mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

- 5 Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA
- 10 sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively).
- 15 Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike,
- 20 four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant
- 25 homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding

predicted amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S. A cDNA splice variant of P501S is provided in SEQ ID NO: 606.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807,

1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the
5 isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were
10 over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-
15 4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively,
20 and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297,
25 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-

4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively. Additional splice variants of P510S are provided in SEQ ID NO: 598 and 599.

The determined cDNA sequences for additional prostate-specific clones isolated during characterization of prostate specific cDNA libraries are provided in SEQ ID NO: 618-689, 691-697 and 709-772. Comparison of these sequences with those in the public databases revealed no significant homologies to any of these sequences.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

- 5 Using gene specific primers, mRNA expression levels for the representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.
- 10 Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was
- 15 used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for
- 20 each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.
- mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung
- 25 tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at
- 30 high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon

and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney,

ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. Subsequent comparison of the sequence of SEQ ID NO: 384 with sequences in the public databases, led to the identification of a full-length cDNA sequence of P1000C (SEQ ID NO: 929), which encodes a 492 amino acid sequence.

Analysis of the amino acid sequence using the PSORT II program led to the identification of a putative transmembrane domain from amino acids 84-100. The cDNA sequence of the open reading frame of P1000C, including the stop codon, is provided in SEQ ID NO: 930, with the open reading frame without the stop codon being
5 provided in SEQ ID NO: 931. The full-length amino acid sequence of P1000C is provided in SEQ ID NO: 932. SEQ ID NO: 933 and 934 represent amino acids 1-100 and 100-492 of P1000C, respectively.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by
10 immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

15 The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver,
20 brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that
25 this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC
POLYPEPTIDES BY PCR-BASED SUBTRACTION

5 A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The
10 resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

 Fifty-nine positive clones were sequenced. Comparison of the DNA
15 sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID
20 NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

 Further studies employing the sequence of SEQ ID NO: 67 as a probe in standard full-length cloning methods, resulted in the isolation of three cDNA sequences
25 which appear to be splice variants of P80 (also known as P704P). These sequences are provided in SEQ ID NO: 699-701.

 Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA
30 sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145,

147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones
5 containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is
10 provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine
15 and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed
20 comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor
25 compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal
30 prostate and prostate tumor, compared to six of twelve other normal tissues tested.

Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and
5 normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-
10 h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in
15 the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

20 mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor
25 and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both microarray technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. The full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding amino acid sequence being provided in SEQ ID NO: 525.

Using computer algorithms, the following regions of P703P were predicted to represent potential HLA A2-binding CTL epitopes: amino acids 164-172 of SEQ ID NO: 525 (SEQ ID NO: 866); amino acids 160-168 of SEQ ID NO: 525 (SEQ ID NO: 867); amino acids 239-247 of SEQ ID NO: 525 (SEQ ID NO: 868); amino acids 118-126 of SEQ ID NO: 525 (SEQ ID NO: 869); amino acids 112-120 of SEQ ID NO: 525 (SEQ ID NO: 870); amino acids 155-164 of SEQ ID NO: 525 (SEQ ID NO: 871); amino acids 117-126 of SEQ ID NO: 525 (SEQ ID NO: 872); amino acids 164-173 of SEQ ID NO: 525 (SEQ ID NO: 873); amino acids 154-163 of SEQ ID NO:

525 (SEQ ID NO: 874); amino acids 163-172 of SEQ ID NO: 525 (SEQ ID NO: 875); amino acids 58-66 of SEQ ID NO: 525 (SEQ ID NO: 876); and amino acids 59-67 of SEQ ID NO: 525 (SEQ ID NO: 877).

P703P was found to show some homology to previously identified
5 proteases, such as thrombin. The thrombin receptor has been shown to be preferentially expressed in highly metastatic breast carcinoma cells and breast carcinoma biopsy samples. Introduction of thrombin receptor antisense cDNA has been shown to inhibit the invasion of metastatic breast carcinoma cells in culture. Antibodies against thrombin receptor inhibit thrombin receptor activation and thrombin-induced platelet
10 activation. Furthermore, peptides that resemble the receptor's tethered ligand domain inhibit platelet aggregation by thrombin. P703P may play a role in prostate cancer through a protease-activated receptor on the cancer cell or on stromal cells. The potential trypsin-like protease activity of P703P may either activate a protease-activated receptor on the cancer cell membrane to promote tumorigenesis or activate a protease-
15 activated receptor on the adjacent cells (such as stromal cells) to secrete growth factors and/or proteases (such as matrix metalloproteinases) that could promote tumor angiogenesis, invasion and metastasis. P703P may thus promote tumor progression and/or metastasis through the activation of protease-activated receptor. Polypeptides and antibodies that block the P703P-receptor interaction may therefore be usefully
20 employed in the treatment of prostate cancer.

To determine whether P703P expression increases with increased severity of Gleason grade, an indicator of tumor stage, quantitative PCR analysis was performed on prostate tumor samples with a range of Gleason scores from 5 to > 8. The mean level of P703P expression increased with increasing Gleason score, indicating that
25 P703P expression may correlate with increased disease severity.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences
30 for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are

provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to
5 normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression
10 in normal prostate.

Further studies led to the isolation of an extended cDNA sequence for P712P (SEQ ID NO: 552). The amino acid sequences encoded by 16 predicted open reading frames present within the sequence of SEQ ID NO: 552 are provided in SEQ ID NO: 553-568.

15 The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these
20 filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted
25 amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice
30 variant of the known gene HoxB13. In contrast, no significant homologies to P714P

were found. Further studies employing the sequence of SEQ ID NO: 334 as a probe in standard full-length cloning methods, resulted in an extended cDNA sequence for P714P. This sequence is provided in SEQ ID NO: 698. This sequence was found to show some homology to the gene that encodes human ribosomal L23A protein.

5 Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

10 Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an
15 ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483. Additional splice variants of P775P are provided in SEQ ID NO: 593-597.

Subsequent studies led to the identification of a genomic region on
20 chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors, and other potential tumor genes may be contained within this region. These studies also led to the identification of a potential
25 open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

Comparison of the clone of SEQ ID NO: 325 (referred to as P558S) with sequences in the GenBank and GeneSeq DNA databases showed that P558S is identical to the prostate-specific transglutaminase gene, which is known to have two forms. The
30 full-length sequences for the two forms are provided in SEQ ID NO: 773 and 774, with

the corresponding amino acid sequences being provided in SEQ ID NO: 775 and 776, respectively. The cDNA sequence of SEQ ID NO: 774 has a 15 pair base insert, resulting in a 5 amino acid insert in the corresponding amino acid sequence (SEQ ID NO: 776). This insert is not present in the sequence of SEQ ID NO: 773.

5 Further studies on P768P (SEQ ID NO: 315) led to the identification of the putative full-length open reading frame (ORF). The cDNA sequence of the ORF with stop codon is provided in SEQ ID NO: 907. The cDNA sequence of the ORF without stop codon is provided in SEQ ID NO: 908, with the corresponding amino acid sequence being provided in SEQ ID NO: 909. This sequence was found to show 86%
10 identity to a rat calcium transporter protein, indicating that P768P may represent a human calcium transporter protein. The locations of transmembrane domains within P768P were predicted using the PSORT II computer algorithm. Six transmembrane domains were predicted at amino acid positions 118-134, 172-188, 211-227, 230-246, 282-298 and 348-364. The amino acid sequences of SEQ ID NO: 910-915 represent
15 amino acids 1-134, 135-188, 189-227, 228-246, 247-298 and 299-511 of P768P, respectively.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

20

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of
25 conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid
30 (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of

0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

5

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

10 A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide
15 restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

20 The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate
25 hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences
30 which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich
5 differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

10 In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for
15 proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA
20 sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant
25 homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most
30 prostate tumors and BPH tissues by a factor of three or greater, with elevated expression

seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

5 Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349,
10 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 11 (SEQ ID NO: 340-349 and 362) were found to show some homology to previously identified sequences. No significant
15 homologies were found to the clones of SEQ ID NO: 350, 351, 353-361, and 363-365.

Comparison of the sequence of SEQ ID NO: 362 with sequences in the GenBank and GeneSeq DNA databases showed that this clone (referred to as P788P) is identical to GeneSeq Accession No. X27262, which encodes a protein found in the GeneSeq protein Accession No. Y00931. The full length cDNA sequence of P788P is
20 shown in Figure 12A (SEQ ID NO: 777), with the corresponding predicted amino acid being shown in Figure 12B (SEQ ID NO: 778). Subsequently, a full-length cDNA sequence for P788P that contains polymorphisms not found in the sequence of SEQ ID NO: 779, was cloned multiple times by PCR amplification from cDNA prepared from several RNA templates from three individuals. This determined cDNA sequence of this
25 polymorphic variant of P788P is provided in SEQ ID NO: 779, with the corresponding amino acid sequence being provided in SEQ ID NO: 780. The sequence of SEQ ID NO: 780 differs from that of SEQ ID NO: 778 by six amino acid residues. The P788P protein has 7 potential transmembrane domains at the C-terminal portion and is predicted to be a plasma membrane protein with an extracellular N-terminal region.

Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

Additional studies on the clone of SEQ ID NO: 354 (referred to as P776P) led to the isolation of an extended cDNA sequence, provided in SEQ ID NO: 569. The determined cDNA sequences of three additional splice variants of P776P are provided in SEQ ID NO: 570-572. The amino acid sequences encoded by two predicted open reading frames (ORFs) contained within SEQ ID NO: 570, one predicted ORF contained within SEQ ID NO: 571, and 11 predicted ORFs contained within SEQ ID NO: 569, are provided in SEQ ID NO: 573-586, respectively. Further studies led to the isolation of the full-length sequence for the clone of SEQ ID NO: 570 (provided in SEQ ID NO: 880). Full-length cloning efforts on the clone of SEQ ID NO: 571 led to the isolation of two sequences (provided in SEQ ID NO: 881 and 882), representing a single clone, that are identical with the exception of a polymorphic insertion/deletion at position 1293. Specifically, the clone of SEQ ID NO: 882 (referred to as clone F1) has a C at position 1293. The clone of SEQ ID NO: 881 (referred to as clone F2) has a single base pair deletion at position 1293. The predicted amino acid sequences encoded by 5 open reading frames located within SEQ ID NO: 880 are provided in SEQ ID NO: 883-887, with the predicted amino acid sequences encoded by the clone of SEQ ID NO: 881 and 882 being provided in SEQ ID NO: 888-893.

Comparison of the cDNA sequences for the clones P767P (SEQ ID NO: 314) and P777P (SEQ ID NO: 350) with sequences in the GenBank human EST database showed that the two clones matched many EST sequences in common,

suggesting that P767P and P777P may represent the same gene. A DNA consensus sequence derived from a DNA sequence alignment of P767P, P777P and multiple EST clones is provided in SEQ ID NO: 587. The amino acid sequences encoded by three putative ORFs located within SEQ ID NO: 587 are provided in SEQ ID NO: 588-590.

5 The clone of SEQ ID NO: 342 (referred to as P789P) was found to show homology to a previously identified gene. The full length cDNA sequence for P789P and the corresponding amino acid sequence are provided in SEQ ID NO: 878 and 879, respectively.

10

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

15 Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were
20 immunized with 100µg of P2S#12 and 120µg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium
25 pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells (5×10^5 /ml) were
30 restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells

(Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed
5 EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with
10 P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

15 6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is
20 derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding
25 using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 μ g/ml were added to
30 cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes,

CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

- 5 Mice expressing the transgene for human HLA A2Kb were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 μ g of P1S #10 and 120 μ g of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single
10 cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2 μ g/ml P1S#10 and 10mg/ml β 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 μ g/ml dextran sulfate and 25 μ g/ml LPS for 3 days). Six days later cells (5×10^5 /ml) were restimulated
15 with 2.5×10^6 /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as
20 shown in Figure 4.

- A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were
25 isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION

WITH A PROSTATE ANTIGEN

The prostate-specific antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg P501S in the vector VR1012 either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed HLA-A2-restricted CTL epitope.

15

EXAMPLE 8

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

20

Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8⁺ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ-interferon ELISPOT assay (*see* Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10⁴ fibroblasts in the presence of 3 µg/ml human β₂-microglobulin and 1 µg/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the

30

fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 9

ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate-specific antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GM-CSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles using autologous fibroblasts

retrovirally transduced to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see above and Lalvani et al., J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN THE PROSTATE-SPECIFIC ANTIGEN P703P

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

Initial studies demonstrating that p5 is a naturally processed epitope were done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100 μg of p5 peptide together with 140 μg of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the

control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte
5 cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with 1 ug/ml p5 peptide and cultured with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures,
10 CTL recognition of p5-pulsed target cells was demonstrated. CTL were additionally shown to recognize human cells transduced to express P703P, demonstrating that p5 is a naturally processed epitope.

Studies identifying a further peptide epitope (referred to as peptide 4) derived from the prostate tumor-specific antigen P703P that is capable of being
15 recognized by CD4 T cells on the surface of cells in the context of HLA class II molecules were carried out as follows. The amino acid sequence for peptide 4 is provided in SEQ ID NO: 781, with the corresponding cDNA sequence being provided in SEQ ID NO: 782.

Twenty 15-mer peptides overlapping by 10 amino acids and derived
20 from the carboxy-terminal fragment of P703P were generated using standard procedures. Dendritic cells (DC) were derived from PBMC of a normal female donor using GM-CSF and IL-4 by standard protocols. CD4 T cells were generated from the same donor as the DC using MACS beads and negative selection. DC were pulsed overnight with pools of the 15-mer peptides, with each peptide at a final concentration
25 of 0.25 microgram/ml. Pulsed DC were washed and plated at 1×10^4 cells/well of 96-well V-bottom plates and purified CD4 T cells were added at 1×10^5 /well. Cultures were supplemented with 60 ng/ml IL-6 and 10 ng/ml IL-12 and incubated at 37 °C. Cultures were restimulated as above on a weekly basis using DC generated and pulsed as above as antigen presenting cells, supplemented with 5 ng/ml IL-7 and 10 u/ml IL-2.
30 Following 4 *in vitro* stimulation cycles, 96 lines (each line corresponding to one well) were tested for specific proliferation and cytokine production in response to the

stimulating pools with an irrelevant pool of peptides derived from mammaglobin being used as a control.

One line (referred to as 1-F9) was identified from pool #1 that demonstrated specific proliferation (measured by 3H proliferation assays) and cytokine production (measured by interferon-gamma ELISA assays) in response to pool #1 of P703P peptides. This line was further tested for specific recognition of the peptide pool, specific recognition of individual peptides in the pool, and in HLA mismatch analyses to identify the relevant restricting allele. Line 1-F9 was found to specifically proliferate and produce interferon-gamma in response to peptide pool #1, and also to peptide 4 (SEQ ID NO: 781). Peptide 4 corresponds to amino acids 126-140 of SEQ ID NO: 327. Peptide titration experiments were conducted to assess the sensitivity of line 1-F9 for the specific peptide. The line was found to specifically respond to peptide 4 at concentrations as low as 0.25 ng/ml, indicating that the T cells are very sensitive and therefore likely to have high affinity for the epitope.

To determine the HLA restriction of the P703P response, a panel of antigen presenting cells (APC) was generated that was partially matched with the donor used to generate the T cells. The APC were pulsed with the peptide and used in proliferation and cytokine assays together with line 1-F9. APC matched with the donor at HLA-DRB0701 and HLA-DQB02 alleles were able to present the peptide to the T cells, indicating that the P703P-specific response is restricted to one of these alleles.

Antibody blocking assays were utilized to determine if the restricting allele was HLA-DR0701 or HLA-DQ02. The anti-HLA-DR blocking antibody L243 or an irrelevant isotype matched IgG2a were added to T cells and APC cultures pulsed with the peptide RMPTVLQCVNVS VVS (SEQ ID NO: 781) at 250 ng/ml. Standard interferon-gamma and proliferation assays were performed. Whereas the control antibody had no effect on the ability of the T cells to recognize peptide-pulsed APC, in both assays the anti-HLA-DR antibody completely blocked the ability of the T cells to specifically recognize peptide-pulsed APC.

To determine if the peptide epitope RMPTVLQCVNVS VVS (SEQ ID NO: 781) was naturally processed, the ability of line 1-F9 to recognize APC pulsed with recombinant P703P protein was examined. For these experiments a number of

recombinant P703P sources were utilized; *E. coli*-derived P703P, Pichia-derived P703P and baculovirus-derived P703P. Irrelevant protein controls used were *E. coli*-derived L3E (a lung-specific antigen) and baculovirus-derived mammaglobin. In interferon-gamma ELISA assays, line 1-F9 was able to efficiently recognize both *E. coli* forms of P703P as well as Pichia-derived recombinant P703P, while baculovirus-derived P703P was recognized less efficiently. Subsequent Western blot analysis revealed that the *E. coli* and Pichia P703P protein preparations were intact while the baculovirus P703P preparation was approximately 75% degraded. Thus, peptide RMPTVLQCVNVS VVS (SEQ ID NO: 781) from P703P is a naturally processed peptide epitope derived from P703P and presented to T cells in the context of HLA-DRB-0701

In further studies, twenty-four 15-mer peptides overlapping by 10 amino acids and derived from the N-terminal fragment of P703P (corresponding to amino acids 27-154 of SEQ ID NO: 525) were generated by standard procedures and their ability to be recognized by CD4 cells was determined essentially as described above. DC were pulsed overnight with pools of the peptides with each peptide at a final concentration of 10 microgram/ml. A large number of individual CD4 T cell lines (65/480) demonstrated significant proliferation and cytokine release (IFN-gamma) in response to the P703P peptide pools but not to a control peptide pool. The CD4 T cell lines which demonstrated specific activity were restimulated on the appropriate pool of P703P peptides and reassayed on the individual peptides of each pool as well as a peptide dose titration of the pool of peptides in a IFN-gamma release assay and in a proliferation assay.

Sixteen immunogenic peptides were recognized by the T cells from the entire set of peptide antigens tested. The amino acid sequences of these peptides are provided in SEQ ID NO: 799-814, with the corresponding cDNA sequences being provided in SEQ ID NO: 783-798, respectively. In some cases the peptide reactivity of the T cell line could be mapped to a single peptide, however some could be mapped to more than one peptide in each pool. Those CD4 T cell lines that displayed a representative pattern of recognition from each peptide pool with a reasonable affinity for peptide were chosen for further analysis (I-1A, -6A; II-4C, -5E; III-6E, IV-4B, -3F, -9B, -10F, V-5B, -4D, and -10F). These CD4 T cells lines were restimulated on the

appropriate individual peptide and reassayed on autologous DC pulsed with a truncated form of recombinant P703P protein made in *E. coli* (a.a. 96 - 254 of SEQ ID NO: 525), full-length P703P made in the baculovirus expression system, and a fusion between influenza virus NS1 and P703P made in *E. coli*. Of the T cell lines tested, line I-1A
5 recognized specifically the truncated form of P703P (*E. coli*) but no other recombinant form of P703P. This line also recognized the peptide used to elicit the T cells. Line 2-4C recognized the truncated form of P703P (*E. coli*) and the full length form of P703P made in baculovirus, as well as peptide. The remaining T cell lines tested were either peptide-specific only (II-5E, II-6F, IV-4B, IV-3F, IV-9B, IV-10F, V-5B and V-4D) or
10 were non-responsive to any antigen tested (V-10F). These results demonstrate that the peptide sequence RPLLANDLMLIKLDE (SEQ ID NO: 814; corresponding to a.a. 110-124 of SEQ ID NO: 525) recognized by the T cell line I-1A, and the peptide sequences SVSESDTIRSISIAS (SEQ ID NO: 811; corresponding to a.a. 125-139 of SEQ ID NO: 525) and ISIASQCPTAGNSCL (SEQ ID NO: 810; corresponding to a.a. 135-149 of
15 SEQ ID NO: 525) recognized by the T cell line II-4C may be naturally processed epitopes of the P703P protein.

In further studies, forty 15-mer peptides overlapping by 10 amino acids and derived spanning amino acids 47 to 254 of P703P (SEQ ID NO: 525) were generated by standard procedures and their ability to be recognized by CD4 cells was
20 determined essentially as described above. DC were prepared from PBMC of a donor having distinct HLA DR and DQ alleles from that used in previous experiments. DC were pulsed overnight with pools of the peptides with each peptide at a final concentration of 0.25 microgram/ml, and each pool containing 10 peptides. Twelve lines were identified that demonstrated specific proliferation and cytokine production
25 (measured in gamma-interferon ELISA assays) in response to the stimulating peptide pool. These lines were further tested for specific recognition of the peptide pool, specific recognition of individual peptides in the pool, and specific recognition of recombinant P703P protein. Lines 3A5H and 3A9H specifically proliferated and produced gamma-interferon in response to recombinant protein and one individual
30 peptide as well as the peptide pool. Following re-stimulation on targets loaded with the specific peptide, only 3A9H responded specifically to targets exposed to lysates of

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fibroblasts infected adenovirus expressing full-length P703P. These results indicates that the line 3A9H can respond to antigenic peptide derived from protein synthesized in mammalian cells. The peptide to which the specific CD4 line responded correspond to amino acids 155-170 of P703P (SEQ ID NO: 943). The DNA sequence for this peptide
5 is provided in SEQ ID NO: 942.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN
IN PROSTATE

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Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino
15 acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively. In further studies, a splice variant of the cDNA sequence of SEQ ID NO: 366 was isolated which was found to contain an additional guanine residue at position 884 (SEQ ID NO: 530), leading to a frameshift in the open reading frame. The determined DNA sequence of this ORF is
20 provided in SEQ ID NO: 531. This frameshift generates a protein sequence (provided in SEQ ID NO: 532) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that
25 B305D is highly expressed in breast tumor, prostate tumor, normal prostate and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach). Using real-time PCR on a panel of prostate tumors, expression of B305D in prostate tumors was shown to increase with increasing

Gleason grade, demonstrating that expression of B305D increases as prostate cancer progresses.

EXAMPLE 12

5 GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH THE PROSTATE-SPECIFIC ANTIGEN P501S

Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996),
10 human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon- γ ELISPOT analysis as described above. Using a panel of HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte
15 cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 μ g/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+
20 T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8+ T cell lines were identified that specifically produced interferon- γ when stimulated with P501S and CD80-transduced autologous
25 fibroblasts. A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- γ in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce
5 Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN-gamma ELISPOT assays against these A2Kb targets transduced with the "library" of P501S fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113,
10 which was unable to stimulate the CTL, thus localizing the epitope to amino acid residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing
15 Jurkat/A2Kb cells versus CTL in an IFN-gamma assay. Only peptides P501S-369(20) and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive
20 epitope.

In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with
25 recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8+ T cells were cultured with autologous CD40 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above
30 background were cloned on autologous EBV-transformed B cells (BLCL), also

transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First, antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding EGFP transduced control BLCL.

A naturally processed, CD8, class I-restricted peptide epitope of P501S was identified as follows. Dendritic Cells (DC) were isolated by Percol gradient followed by differential adherence, and cultured for 5 days in the presence of RPMI medium containing 1% human serum, 50ng/ml GM-CSF and 30ng/ml IL-4. Following culture, DC were infected for 24 hours with P501S-expressing adenovirus at an MOI of 10 and matured for an additional 24 hours by the addition of 2ug/ml CD40 ligand. CD8 cells were enriched for by the subtraction of CD4+, CD14+ and CD16+ populations from PBMC with magnetic beads. Priming cultures containing 10,000 P501S-expressing DC and 100,000 CD8+ T cells per well were set up in 96-well V-bottom plates with RPMI containing 10% human serum, 5ng/ml IL-12 and 10ng/ml IL-6. Cultures were stimulated every 7 days using autologous fibroblasts retrovirally transduced to express P501S and CD80, and were treated with IFN-gamma for 48-72 hours to upregulate MHC Class I expression. 10u/ml IL-2 was added at the time of stimulation and on days 2 and 5 following stimulation. Following 4 stimulation cycles, one P501S-specific CD8+ T cell line (referred to as 2A2) was identified that produced IFN-gamma in response to IFN-gamma-treated P501S/CD80 expressing autologous fibroblasts, but not in response to IFN-gamma-treated P703P/CD80 expressing autologous fibroblasts in a γ -IFN Elispot assay. Line 2A2 was cloned in 96-well plates with 0.5 cell/well or 2 cells/well in the presence of 75,000 PBMC/well, 10,000 B-LCL/well, 30ng/ml OKT3 and 50u/ml IL-2. Twelve clones were isolated that showed strong P501S specificity in response to transduced fibroblasts.

Fluorescence activated cell sorting (FACS) analysis was performed on P501S-specific clones using CD3-, CD4- and CD8-specific antibodies conjugated to PercP, FITC and PE respectively. Consistent with the use of CD8 enriched T cells in the priming cultures, P5401S-specific clones were determined to be CD3+, CD8+ and CD4-.

To identify the relevant P501S epitope recognized by P501S specific CTL, pools of 18-20 mer or 30-mer peptides that spanned the majority of the amino acid sequence of P501S were loaded onto autologous B-LCL and tested in γ -IFN Elispot assays for the ability to stimulate two P501S-specific CTL clones, referred to as 4E5 and 4E7. One pool, composed of five 18-20 mer peptides that spanned amino acids 411-486 of P501S (SEQ ID NO: 113), was found to be recognized by both P501S-specific clones. To identify the specific 18-20 mer peptide recognized by the clones, each of the 18-20 mer peptides that comprised the positive pool were tested individually in γ -IFN Elispot assays for the ability to stimulate the two P501S-specific CTL clones, 4E5 and 4E7. Both 4E5 and 4E7 specifically recognized one 20-mer peptide (SEQ ID NO: 853; cDNA sequence provided in SEQ ID NO: 854) that spanned amino acids 453-472 of P501S. Since the minimal epitope recognized by CD8+ T cells is almost always either a 9 or 10-mer peptide sequence, 10-mer peptides that spanned the entire sequence of SEQ ID NO: 853 were synthesized that differed by 1 amino acid. Each of these 10-mer peptides was tested for the ability to stimulate two P501S-specific clones, (referred to as 1D5 and 1E12). One 10-mer peptide (SEQ ID NO: 855; cDNA sequence provided in SEQ ID NO: 856) was identified that specifically stimulated the P501S-specific clones. This epitope spans amino acids 463-472 of P501S. This sequence defines a minimal 10-mer epitope from P501S that can be naturally processed and to which CTL responses can be identified in normal PBMC. Thus, this epitope is a candidate for use as a vaccine moiety, and as a therapeutic and/or diagnostic reagent for prostate cancer.

To identify the class I restriction element for the P501S-derived sequence of SEQ ID NO: 855, HLA blocking and mismatch analyses were performed. In γ -IFN Elispot assays, the specific response of clones 4A7 and 4E5 to P501S-transduced autologous fibroblasts was blocked by pre-incubation with 25ug/ml W6/32 (pan-Class I blocking antibody) and B1.23.2 (HLA-B/C blocking antibody). These results

demonstrate that the SEQ ID NO: 855-specific response is restricted to an HLA-B or HLA-C allele.

For the HLA mismatch analysis, autologous B-LCL (HLA-A1,A2,B8,B51, Cw1, Cw7) and heterologous B-LCL (HLA-A2,A3,B18,B51,Cw5,Cw14) that share the HLAB51 allele were pulsed for one hour with 20ug/ml of peptide of SEQ ID NO: 855, washed, and tested in γ -IFN Elispot assays for the ability to stimulate clones 4A7 and 4E5. Antibody blocking assays with the B1.23.2 (HLA-B/C blocking antibody) were also performed. SEQ ID NO: 855-specific response was detected using both the autologous (D326) and heterologous (D107) B-LCL, and furthermore the responses were blocked by pre-incubation with 25ug/ml of B1.23.2 HLA-B/C blocking antibody. Together these results demonstrate that the P501S-specific response to the peptide of SEQ ID NO: 855 is restricted to the HLA-B51 class I allele. Molecular cloning and sequence analysis of the HLA-B51 allele from D3326 revealed that the HLA-B51 subtype of D326 is HLA-B51011.

Based on the 10-mer P501S-derived epitope of SEQ ID NO: 855, two 9-mers with the sequences of SEQ ID NO: 857 and 858 were synthesized and tested in Elispot assays for the ability to stimulate two P501S-specific CTL clones derived from line 2A2. The 10-mer peptide of SEQ ID NO: 855, as well as the 9-mer peptide of SEQ ID NO: 858, but not the 9-mer peptide of SEQ ID NO: 857, were capable of stimulating the P501S-specific CTL to produce IFN-gamma. These results demonstrate that the peptide of SEQ ID NO: 858 is a 9-mer P501S-derived epitope recognized by P501S-specific CTL. The DNA sequence encoding the epitope of SEQ ID NO: 858 is provided in SEQ ID NO: 859.

To identify the class I restricting allele for the P501S-derived peptide of SEQ ID NO: 855 and 858 specific response, each of the HLA B and C alleles were cloned from the donor used in the *in vitro* priming experiment. Sequence analysis indicated that the relevant alleles were HLA-B8, HLA-B51, HLA-Cw01 and HLA-Cw07. Each of these alleles were subcloned into an expression vector and co-transfected together with the P501S gene into VA-13 cells. Transfected VA-13 cells were then tested for the ability to specifically stimulate the P501S-specific CTL in ELISPOT assays. VA-13 cells transfected with P501S and HLA-B51 were capable of

stimulating the P501S-specific CTL to secrete gamma-IFN. VA-13 cells transfected with HLA-B51 alone or P501S + the other HLA-alleles were not capable of stimulating the P501S-specific CTL. These results demonstrate that the restricting allele for the P501S-specific response is the HLAB51 allele. Sequence analysis revealed that the
5 subtype of the relevant restricting allele is HLA-B51011.

To determine if the P501S-specific CTL could recognize prostate tumor cells that express P501S, the P501S-positive lines LnCAP and CRL2422 (both expressing "moderate" amounts of P501S mRNA and protein), and PC-3 (expressing low amounts of P501S mRNA and protein), plus the P501S-negative cell line DU-145
10 were retrovirally transduced with the HLA-B51011 allele that was cloned from the donor used to generate the P501S-specific CTL. HLA-B51011- or EGFP-transduced and selected tumor cells were treated with gamma-interferon and androgen (to upregulate stimulatory functions and P501S, respectively) and used in gamma-interferon Elispot assays with the P501S-specific CTL clones 4E5 and 4E7. Untreated
15 cells were used as a control.

Both 4E5 and 4E7 efficiently and specifically recognized LnCAP and CRL2422 cells that were transduced with the HLA-B51011 allele, but not the same cell lines transduced with EGFP. Additionally, both CTL clones specifically recognized PC-3 cells transduced with HLA-B51011, but not the P501S-negative tumor cell line
20 DU-145. Treatment with gamma-interferon or androgen did not enhance the ability of CTL to recognize tumor cells. These results demonstrate that P501S-specific CTL, generated by *in vitro* whole gene priming, specifically and efficiently recognize prostate tumor cell lines that express P501S.

A naturally processed CD4 epitope of P501S was identified as follows.

25 CD4 cells specific for P501S were prepared as described above. A series of 16 overlapping peptides were synthesized that spanned approximately 50% of the amino terminal portion of the P501S gene (amino acids 1- 325 of SEQ ID NO: 113). For priming, peptides were combined into pools of 4 peptides, pulsed at 4 µg/ml onto dendritic cells (DC) for 24 hours, with TNF-alpha. DC were then washed and mixed
30 with negatively selected CD4+ T cells in 96 well U-bottom plates. Cultures were re-stimulated weekly on fresh DC loaded with peptide pools. Following a total of 4

stimulation cycles, cells were rested for an additional week and tested for specificity to APC pulsed with peptide pools using γ -IFN ELISA and proliferation assays. For these assays, adherent monocytes loaded with either the relevant peptide pool at 4ug/ml or an irrelevant peptide at μ g/ml were used as APC. T cell lines that demonstrated either
5 specific cytokine secretion or proliferation were then tested for recognition of individual peptides that were present in the pool. T cell lines could be identified from pools A and B that recognized individual peptides from these pools.

From pool A, lines AD9 and AE10 specifically recognized peptide 1 (SEQ ID NO: 862), and line AF5 recognized peptide 39 (SEQ ID NO: 861). From pool
10 B, line BC6 could be identified that recognized peptide 58 (SEQ ID NO: 860). Each of these lines were stimulated on the specific peptide and tested for specific recognition of the peptide in a titration assay as well as cell lysates generated by infection of HEK 293 cells with adenovirus expressing either P501S or an irrelevant antigen. For these assays, APC-adherent monocytes were pulsed with either 10, 1, or 0.1 μ g/ml individual P501S
15 peptides, and DC were pulsed overnight with a 1:5 dilution of adenovirally infected cell lysates. Lines AD9, AE10 and AF5 retained significant recognition of the relevant P501S-derived peptides even at 0.1 mg/ml. Furthermore, line AD9 demonstrated significant (8.1 fold stimulation index) specific activity for lysates from adenovirus-P501S infected cells. These results demonstrate that high affinity CD4 T cell lines can
20 be generated toward P501S-derived epitopes, and that at least a subset of these T cells specific for the P501S derived sequence of SEQ ID NO: 862 are specific for an epitope that is naturally processed by human cells. The DNA sequences encoding the amino acid sequences of SEQ ID NO: 860-862 are provided in SEQ ID NO: 863-865, respectively.

25 To further characterize the P501S-specific activity of AD9, the line was cloned using anti-CD3. Three clones, referred to as 1A1, 1A9 and 1F5, were identified that were specific for the P501S-1 peptide (SEQ ID NO: 862). To determine the HLA restriction allele for the P501S-specific response, each of these clones was tested in class II antibody blocking and HLA mismatch assays using proliferation and gamma-
30 interferon assays. In antibody blocking assays and measuring gamma-interferon production using ELISA assays, the ability of all three clones to recognize peptide

pulsed APC was specifically blocked by co-incubation with either a pan-class II blocking antibody or a HLA-DR blocking antibody, but not with a HLA-DQ or an irrelevant antibody. Proliferation assays performed simultaneously with the same cells confirmed these results. These data indicate that the P501S-specific response of the clones is restricted by an HLA-DR allele. Further studies demonstrated that the restricting allele for the P501S-specific response is HLA-DRB1501.

EXAMPLE 13

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

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Table ISummary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-Iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein. (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other

normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 (also referred to as P553S) showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

Subsequent full-length cloning studies on P553S, using standard techniques, revealed that this clone is an incomplete spliced form of P501S. The determined cDNA sequences for four splice variants of P553S are provided in SEQ ID NO: 702-705. An amino acid sequence encoded by SEQ ID NO: 705 is provided in SEQ ID NO: 706. The cDNA sequence of SEQ ID NO: 702 was found to contain two open reading frames (ORFs). The amino acid sequences encoded by these two ORFs are provided in SEQ ID NO: 707 and 708.

EXAMPLE 14

25

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table IIProstate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

- 5 Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the
- 10 Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters
- 15 (see Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

5 The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels
10 of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes
15 generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

 Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The
20 sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

Table IV

Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57

439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

Further studies on the clone of SEQ ID NO: 407 (also referred to as P1020C) led to the isolation of an extended cDNA sequence provided in SEQ ID NO: 591. This extended cDNA sequence was found to contain an open reading frame that
5 encodes the predicted amino acid sequence of SEQ ID NO: 592. The P1020C cDNA and amino acid sequences were found to show some similarity to the human endogenous retroviral HERV-K pol gene and protein.

EXAMPLE 15

10 FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above
15 was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-460 represent novel genes. The others (SEQ ID NO: 454-
20 458 and 461-467) correspond to known sequences. Comparison of the determined

cDNA sequence of SEQ ID NO: 461 with sequences in the Genbank database using the BLAST program revealed homology to the previously identified transmembrane protease serine 2 (TMPRSS2). The full-length cDNA sequence for this clone is provided in SEQ ID NO: 894, with the corresponding amino acid sequence being
5 provided in SEQ ID NO: 895. The cDNA sequence encoding the first 209 amino acids of TMPRSS2 is provided in SEQ ID NO: 896, with the first 209 amino acids being provided in SEQ ID NO: 897.

The sequence of SEQ ID NO: 462 (referred to as P835P) was found to correspond to the previously identified clone FLJ13518 (Accession AK023643; SEQ ID
10 NO: 917), which had no associated open reading frame (ORF). This clone was used to search the Geneseq DNA database and matched a clone previously identified as a G protein-coupled receptor protein (DNA Geneseq Accession A09351; amino acid Geneseq Accession Y92365), that is characterized by the presence of seven transmembrane domains. The sequences of fragments between these domains are
15 provided in SEQ ID NO: 921-928, with SEQ ID NO: 921, 923, 925 and 927 representing extracellular domains and SEQ ID NO: 922, 924, 926 and 928 representing intracellular domains. SEQ ID NO: 921-928 represent amino acids 1-28, 53-61, 83-103, 124-143, 165-201, 226-238, 263-272 and 297-381, respectively, of P835P. The full-length cDNA sequence for P835P is provided in SEQ ID NO: 916. The cDNA
20 sequence of the open reading frame for P835P, including stop codon, is provided in SEQ ID NO: 918, with the open reading frame without stop codon being provided in SEQ ID NO: 919 and the corresponding amino acid sequence being provided in SEQ ID NO: 920.

25

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P
30 fragment described above. One million colonies were plated on LB/Ampicillin plates.

Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin Elmer/Applied Biosystems Division Sequencer. Four sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene. Subsequent comparison of the cDNA sequences of P710P with those in Genbank revealed homology to the DD3 gene (Genbank accession numbers AF103907 & AF103908). The cDNA sequence of DD3 is provided in SEQ ID NO: 690.

EXAMPLE 17

PROTEIN EXPRESSION OF PROSTATE-SPECIFIC ANTIGENS

This example describes the expression and purification of prostate-specific antigens in *E. coli*, baculovirus and mammalian cells.

a) Expression of P501S in *E. coli*

Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113) downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 µl 10X Pfu buffer, 1 µl 20 mM dNTPs, 1 µl each of the PCR primers at 10 µM concentration, 40 µl water, 1 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min, and lastly by 1 cycle of 72°C for 10 min. The PCR product was

cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus *E. coli* (Stratagene) and grown overnight in LB broth with kanamycin. The
5 resulting culture was induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A (Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression
10 was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen
15 Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as
20 Ra12-P501S-N) was confirmed by DNA sequencing.

The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands were also observed, probably due to
25 aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of
30 the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) was prepared as follows. P501S

DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The
5 sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C
10 fusion was used for expression in BL21CodonPlus induced by CE6 phage.

A fusion construct comprising a fragment of P501S (amino acids 36-298 of SEQ ID NO: 113) located down-stream of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 848) was prepared as follows. P501S DNA was used to perform PCR using the primers AW042 (SEQ ID NO: 849) and AW053 (SEQ ID NO: 850). AW042 is a sense
15 cloning primer that contains a EcoRI site. AW053 is an antisense primer with stop and Xho I sites. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the EcoRI and Xho I sites. The resulting fusion construct (referred to as Ra12-P501S-E2) was expressed in B834 (DE3) pLys S *E. coli* host cells in TB media for 2 h at room temperature. Expressed protein
20 was purified by washing the inclusion bodies and running on a Ni-NTA column. The purified protein stayed soluble in buffer containing 20 mM Tris-HCl (pH 8), 100 mM NaCl, 10 mM β -Me and 5% glycerol. The determined cDNA and amino acid sequences for the expressed fusion protein are provided in SEQ ID NO: 851 and 852, respectfully.

25 **b) Expression of P501S in Baculovirus**

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the

manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant protein.

c) Expression of P501S in mammalian cells

Full-length P501S (553 amino acids; SEQ ID NO: 113) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The

Fugene/DNA mixture was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 µl of GenePorter was diluted in 500 µl of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 µg of plasmid DNA that was diluted in 500 µl of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antisera raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

d) Expression of P703P in Baculovirus

The cDNA for full-length P703P-DE5 (SEQ ID NO: 326), together with several flanking restriction sites, was obtained by digesting the plasmid pCDNA703 with restriction endonucleases Xba I and Hind III. The resulting restriction fragment (approx. 800 base pairs) was ligated into the transfer plasmid pFastBacI which was digested with the same restriction enzymes. The sequence of the insert was confirmed by DNA sequencing. The recombinant transfer plasmid pFBP703 was used to make recombinant bacmid DNA and baculovirus using the Bac-To-Bac Baculovirus expression system (BRL Life Technologies). High Five cells were infected with the recombinant virus BVP703, as described above, to obtain recombinant P703P protein.

e) Expression of P788P in *E. Coli*

A truncated, N-terminal portion, of P788P (residues 1-644 of SEQ ID NO: 777; referred to as P788P-N) fused with a C-terminal 6xHis Tag was expressed in *E. coli* as follows. P788P cDNA was amplified using the primers AW080 and AW081 (SEQ ID NO: 815 and 816). AW080 is a sense cloning primer with an NdeI site. AW081 is an antisense cloning primer with a XhoI site. The PCR-amplified P788P, as well as the vector pCRX1, were digested with NdeI and XhoI. Vector and insert were ligated and transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. P788P-N clone #6 was confirmed to be identical to the designed construct. The expression construct P788P-N #6/pCRX1 was transformed into *E. coli* BL21 CodonPlus-RIL competent cells. After induction, most of the cells grew well, achieving OD600 of greater than 2.0 after 3 hr. Coomassie stained SDS-PAGE showed an over-expressed band at about 75 kD. Western blot analysis using a 6xHisTag antibody confirmed the band was P788P-N. The determined cDNA sequence for P788P-N is provided in SEQ ID NO: 817, with the corresponding amino acid sequence being provided in SEQ ID NO: 818.

f) Expression of P510S in *E. coli*

The P510S protein has 9 potential transmembrane domains and is predicted to be located at the plasma membrane. The C-terminal protein of this protein, as well as the predicted third extracellular domain of P510S were expressed in *E. coli* as follows.

The expression construct referred to as Ra12-P501S-C was designed to have a 6 HisTag at the N-terminal end, followed by the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 819) and then the C-terminal portion of P510S (amino residues 1176-1261 of SEQ ID NO: 538). Full-length P510S was used to amplify the P510S-C fragment by PCR using the primers AW056 and AW057 (SEQ ID NO: 820 and 821, respectively). AW056 is a sense cloning primer with an EcoRI site. AW057 is an antisense primer with stop and XhoI sites. The amplified P501S fragment and Ra12/pCRX1 were digested with EcoRI and XhoI and then purified. The insert and

vector were ligated together and transformed into NovaBlue. Colonies were randomly screened for insert and sequences. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. A mini-induction screen was performed to optimize the expression conditions. After induction
5 the cells grew well, achieving OD 600 nm greater than 2.0 after 3 hours. Coomassie stain SDS-PAGE showed a highly over-expressed band at approx. 30 kD. Though this is higher than the expected molecular weight, western blot analysis was positive, showing this band to be the His tag-containing protein. The optimized culture conditions are as follows. Dilute overnight culture/daytime culture (LB + kanamycin +
10 chloramphenicol) into 2xYT (with kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2xYT. Allow to grow at 37 °C until OD600 = 0.6. Take an aliquot out as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3 sample, spin down cells and store at -80 °C. The determined cDNA and amino acid sequences for the Ra12-P510S-C construct are provided in SEQ ID NO: 822 and 825,
15 respectively.

The expression construct P510S-C was designed to have a 5' added start codon and a glycine (GGA) codon and then the P510S C terminal fragment followed by the in frame 6x histidine tag and stop codon from the pET28b vector. The cloning strategy is similar to that used for Ra12-P510S-C, except that the PCR primers
20 employed were those shown in SEQ ID NO: 828 and 829, respectively and the NcoI/XhoI cut in pET28b was used. The primer of SEQ ID NO: 828 created a 5' NcoI site and added a start codon. The antisense primer of SEQ ID NO: 829 creates a XhoI site on P510S C terminal fragment. Clones were confirmed by sequencing. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3)
25 CodonPlus-RIL competent cells. An OD600 of greater than 2.0 was obtained 30 hours after induction. Coomassie stained SDS-PAGE showed an over-expressed band at about 11 kD. Western blot analysis confirmed that the band was P510S-C, as did N-terminal protein sequencing. The optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (+
30 kanamycin and chloramphenicol) at a ratio of 25 mL culture to 1 liter 2x YT, and allow

to grow at 37 °C until an OD 600 of about 0.5 is reached. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P510S-C construct are shown in SEQ ID NO: 823 and 826, respectively.

5 The predicted third extracellular domain of P510S (P510S-E3; residues 328-676 of SEQ ID NO: 538) was expressed in *E. coli* as follows. The P510S fragment was amplified by PCR using the primers shown in SEQ ID NO: 830 and 831. The primer of SEQ ID NO: 830 is a sense primer with an NdeI site for use in ligating into pPDM. The primer of SEQ ID NO: 831 is an antisense primer with an added XhoI site
10 for use in ligating into pPDM. The resulting fragment was cloned to pPDM at the NdeI and XhoI sites. Clones were confirmed by sequencing. For protein expression, the clone was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. After induction, an OD600 of greater than 2.0 was achieved after 3 hours. Coomassie stained SDS-PAGE showed an over-expressed band at about 39 kD, and N-terminal sequencing
15 confirmed the N-terminal to be that of P510S-E3. Optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2x YT. Allow to grow at 37 °C until OD 600 equals 0.6. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3
20 sample, spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P501S-E3 construct are provided in SEQ ID NO: 824 and 827, respectively.

g) Expression of P775S in *E. Coli*

25 The antigen P775P contains multiple open reading frames (ORF). The third ORF, encoding the protein of SEQ ID NO: 483, has the best motif score. An expression fusion construct containing the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 819) and P775P-ORF3 with an N-terminal 6x HisTag was prepared as follows. P775P-ORF3 was amplified using the sense PCR primers of SEQ ID NO: 832 and the anti-sense PCR primer of SEQ ID NO: 833. The PCR amplified fragment of P775P and

Ra12/pCRX1 were digested with the restriction enzymes EcoRI and XhoI. Vector and insert were ligated and then transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. A clone having the desired sequence was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. Two hours after induction, the cell density peaked at OD600 of approximately 1.8. Coomassie stained SDS-PAGE showed an over-expressed band at about 31 kD. Western blot using 6x HisTag antibody confirmed that the band was Ra12-P775P-ORF3. The determined cDNA and amino acid sequences for the fusion construct are provided in SEQ ID NO: 834 and 835, respectively.

H) Expression of a P703P His tag fusion protein in *E. coli*

The cDNA for the coding region of P703P was prepared by PCR using the primers of SEQ ID NO: 836 and 837. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P703P are provided in SEQ ID NO: 838 and 839, respectively.

I) Expression of a P705P His tag fusion protein in *E. coli*

The cDNA for the coding region of P705P was prepared by PCR using the primers of SEQ ID NO: 840 and 841. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P705P are provided in SEQ ID NO: 842 and 843, respectively.

J) Expression of a P711P His tag fusion protein in *E. coli*

The cDNA for the coding region of P711P was prepared by PCR using the primers of SEQ ID NO: 844 and 845. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P711P are provided in SEQ ID NO: 846 and 847, respectively.

K) Expression of P767P in *E. coli*

The full-length coding region of P767P (amino acids 2-374 of SEQ ID NO: 590) was amplified by PCR using the primers PDM-468 and PDM-469 (SEQ ID NO: 935 and 936, respectively). DNA amplification was performed using 10 µl 10X Pfu buffer, 1 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM concentration, 83 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 20 sec, 66°C for 15 sec and by 72°C for 2 min., and lastly by 1 cycle of 72°C for 4 min. The PCR product was digested with XhoI and cloned into a modified pET28 vector with a histidine tag in frame on the 5' end that was digested with Eco72I and XhoI. The construct was confirmed to be correct through sequence analysis and transformed into *E. coli* BL21 pLysS and BL21 CodonPlus RP cells. The cDNA coding region for the recombinant B767P protein is provided in SEQ ID NO: 938, with the corresponding amino acid sequence being provided in SEQ ID NO: 941. The full-length P767P did not express at high enough levels for detection or purification.

A truncated coding region of P767P (referred to as B767P-B; amino acids 47-374 of SEQ ID NO: 590) was amplified by PCR using the primers PDM-573 and PDM-469 (SEQ ID NO: 937 and 936, respectively) and the PCR conditions described above for full-length P767P. The PCR product was digested with XhoI and cloned into the modified pET28 vector that was digested with Eco72I and XhoI. The

construct was confirmed to be correct through sequence analysis and transformed into *E. coli* BL21 pLysS and BL21 CodonPlus RP cells. The protein was found to be expressed in the inclusion body pellet. The coding region for the expressed B767P-B protein is provided in SEQ ID NO: 939, with the corresponding amino acid sequence
5 being provided in SEQ ID NO: 940.

EXAMPLE 18

PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

10

a) Preparation and Characterization of Polyclonal Antibodies against P703P, P504S and P509S

Polyclonal antibodies against P703P, P504S and P509S were prepared as follows.

15

Each prostate tumor antigen expressed in an *E. coli* recombinant expression system was grown overnight in LB broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml to 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nm) of the culture reached 0.4-0.6, the cells were
20 induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty ml of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run
25 through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed

inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

As a final purification step, a strong anion exchange resin such as HiPrepQ (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off the column with a increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The proteins were then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

Four hundred micrograms of each prostate antigen was combined with 100 micrograms of muramyl dipeptide (MDP). Every four weeks rabbits were boosted with 100 micrograms mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animal was bled. Sera was generated by incubating the blood at 4°C for 12-4 hours followed by centrifugation.

Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) of recombinant protein at 4 °C for 20 hours. 250 microliters of BSA blocking buffer was added to the wells and incubated at room temperature for 2 hours. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at room temperature for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at room temperature for 30 min. Plates were again

washed as described above and 100 microliters of TMB microwell peroxidase substrate was added to each well. Following a 15 min incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H₂SO₄ and read immediately at 450 nm. All polyclonal antibodies showed immunoreactivity to the appropriate antigen.

b) Preparation and Characterization of Antibodies against P501S

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO: 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody component were sacrificed and spleen cells were used to generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant ($\mu\text{g/ml}$)
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

5 The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis. Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1 $\mu\text{g/ml}$, followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using

10 an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-

15 LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8 as a control antigen and either fixed and permeabilized as described

above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity than DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr. HRP-labeled anti-

mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L)Affinipure F(ab') fragment (Jackson ImmunoResearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors,

5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

c) Preparation and Characterization of Antibodies against P503S

5 A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at
10 Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

15

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows. The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further 15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using at ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to cell surface epitopes. Cells stably transfected with a control plasmid were employed as a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur

fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall bladder, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with each of the anti-P503S monoclonal antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

d) Preparation and Characterization of Antibodies against P703P

Rabbits were immunized with either a truncated (P703Ptr1; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptr1 attached to a solid support. Rabbit monoclonal antibodies were isolated using SLAM

technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk^{-/-} cells either untransfected or transfected with a plasmid expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure

specificity, lysates from HEK293 cells stably transfected with a control plasmid were also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using
5 anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues tested (breast tumor, lung tumor and normal kidney).

e) Preparation and Characterization of Antibodies against P504S

Full-length P504S (SEQ ID NO: 108) was expressed and purified from
10 bacteria essentially as described above for P501S and employed to raise rabbit monoclonal antibodies using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). The anti-P504S monoclonal antibody 13H4 was shown by Western blot to bind to both expressed recombinant P504S and to native P504S in tumor cells.

15 Immunohistochemical studies using 13H4 to assess P504S expression in various prostate tissues were performed as described above. A total of 104 cases, including 65 cases of radical prostatectomies with prostate cancer (PC), 26 cases of prostate biopsies and 13 cases of benign prostate hyperplasia (BPH), were stained with the anti-P504S monoclonal antibody 13H4. P504S showed strongly cytoplasmic
20 granular staining in 64/65 (98.5%) of PCs in prostatectomies and 26/26 (100%) of PCs in prostatic biopsies. P504S was stained strongly and diffusely in carcinomas (4+ in 91.2% of cases of PC; 3+ in 5.5%; 2+ in 2.2% and 1+ in 1.1%) and high grade prostatic intraepithelial neoplasia (4+ in all cases). The expression of P504S did not vary with Gleason score. Only 17/91 (18.7%) of cases of NP/BPH around PC and 2/13 (15.4%) of
25 BPH cases were focally (1+, no 2+ to 4+ in all cases) and weakly positive for P504S in large glands. Expression of P504S was not found in small atrophic glands, postatrophic hyperplasia, basal cell hyperplasia and transitional cell metaplasia in either biopsies or prostatectomies. P504S was thus found to be over-expressed in all Gleason scores of prostate cancer (98.5 to 100% of sensitivity) and exhibited only focal positivities in

large normal glands in 19/104 of cases (82.3% of specificity). These findings indicate that P504S may be usefully employed for the diagnosis of prostate cancer.

EXAMPLE 19

5. CHARACTERIZATION OF CELL SURFACE EXPRESSION AND CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine
10 the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow
15 the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains.
20 Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as described by Tusnady and Simon (Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol.* 283:489-506, 1998).

25 Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519, which is identical to the peptide of SEQ ID NO: 518 with the exception of the
30 substitution of the histidine with an asparagine, was synthesized as described above. A

Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether.

- 5 The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described
10 above.

- Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 µg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell
15 sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and
20 stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (*i.e.*, intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

- 25 To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1 complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun
30 at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C.

Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g (internal membrane) fraction and also in the 100,000g (plasma membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 µg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng - 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of

SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above. To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

In further studies, mouse monoclonal antibodies were raised against amino acids 296 to 322 to P501S, which are predicted to be in an extracellular domain. A/J mice were immunized with P501S/adenovirus, followed by subsequent boosts with an *E. coli* recombinant protein, referred to as P501N, that contains amino acids 296 to 322 of P501S, and with peptide 296-322 (SEQ ID NO: 898) coupled with KLH. The mice were subsequently used for splenic B cell fusions to generate anti-peptide hybridomas. The resulting 3 clones, referred to as 4F4 (IgG1,kappa), 4G5 (IgG2a,kappa) and 9B9 (IgG1,kappa), were grown for antibody production. The 4G5 mAb was purified by passing the supernatant over a Protein A-sepharose column,

followed by antibody elution using 0.2M glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8, and buffer exchanged into PBS.

For ELISA analysis, 96 well plates were coated with P501S peptide 296-322 (referred to as P501-long), an irrelevant P775 peptide, P501S-N, P501TR2, P501S-long-KLH, P501S peptide 306-319 (referred to as P501-short)-KLH, or the irrelevant peptide 2073-KLH, all at a concentration of 2 ug/ml and allowed to incubate for 60 minutes at 37 °C. After coating, plates were washed 5X with PBS + 0.1% Tween and then blocked with PBS, 0.5% BSA, 0.4% Tween20 for 2 hours at room temperature. Following the addition of supernatants or purified mAb, the plates were incubated for 60 minutes at room temperature. Plates were washed as above and donkey anti-mouse IgHRP-linked secondary antibody was added and incubated for 30 minutes at room temperature, followed by a final washing as above. TMB peroxidase substrate was added and incubated 15 minutes at room temperature in the dark. The reaction was stopped by the addition of 1N H₂SO₄ and the OD was read at 450 nM. All three hybrid clones secreted mAb that recognized peptide 296-322 and the recombinant protein P501N.

For FACS analysis, HEK293 cells were transiently transfected with a P501S/VR1012 expression constructs using Fugene 6 reagent. After 2 days of culture, cells were harvested and washed, then incubated with purified 4G5 mAb for 30 minutes on ice. After several washes in PBS, 0.5% BSA, 0.01% azide, goat anti-mouse Ig-FITC was added to the cells and incubated for 30 minutes on ice. Cells were washed and resuspended in wash buffer including 1% propidium iodide and subjected to FACS analysis. The FACS analysis confirmed that amino acids 296-322 of P501S are in an extracellular domain and are cell surface expressed.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server

(<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al.* *Science* 274:1371-1374, 1996 and Berthon *et al. Am. J. Hum. Genet.* 62:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

EXAMPLE 20

REGULATION OF EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10

Steroid (androgen) hormone modulation is a common treatment modality in prostate cancer. The expression of a number of prostate tissue-specific antigens have previously been demonstrated to respond to androgen. The responsiveness of the prostate-specific antigen P501S to androgen treatment was examined in a tissue culture system as follows.

15

Cells from the prostate tumor cell line LNCaP were plated at 1.5×10^6 cells/T75 flask (for RNA isolation) or 3×10^5 cells/well of a 6-well plate (for FACS analysis) and grown overnight in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum (BRL Life Technologies, Gaithersburg, MD). Cell culture was continued for an additional 72 hours in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum, with 1 nM of the synthetic androgen Methyltrienolone (R1881; New England Nuclear) added at various time points. Cells were then harvested for RNA isolation and FACS analysis at 0, 1, 2, 4, 8, 16, 24, 28 and 72-hours post androgen addition. FACS analysis was performed using the anti-P501S antibody 10E3-G4-D3 and permeabilized cells.

25

For Northern analysis, 5-10 micrograms of total RNA was run on a formaldehyde denaturing gel, transferred to Hybond-N nylon membrane (Amersham Pharmacia Biotech, Piscataway, NJ), cross-linked and stained with methylene blue. The filter was then prehybridized with Church's Buffer (250 mM Na_2HPO_4 , 70 mM H_3PO_4 , 1 mM EDTA, 1% SDS, 1% BSA in pH 7.2) at 65 °C for 1 hour. P501S DNA was

30

labeled with ^{32}P using High Prime random-primed DNA labeling kit (Boehringer Mannheim). Unincorporated label was removed using MicroSpin S300-HR columns (Amersham Pharmacia Biotech). The RNA filter was then hybridized with fresh Church's Buffer containing labeled cDNA overnight, washed with 1X SCP (0.1 M NaCl, 0.03 M $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 0.001 M Na_2EDTA), 1% sarkosyl (n-lauroylsarcosine) and exposed to X-ray film.

Using both FACS and Northern analysis, P501S message and protein levels were found to increase in response to androgen treatment.

10

EXAMPLE 21

PREPARATION OF FUSION PROTEINS OF PROSTATE-SPECIFIC ANTIGENS

The example describes the preparation of a fusion protein of the prostate-specific antigen P703P and a truncated form of the known prostate antigen PSA. The truncated form of PSA has a 21 amino acid deletion around the active serine site. The expression construct for the fusion protein also has a restriction site at 3' end, immediately prior to the termination codon, to aid in adding cDNA for additional antigens.

The full-length cDNA for PSA was obtained by RT-PCR from a pool of RNA from human prostate tumor tissues using the primers of SEQ ID NO: 607 and 608, and cloned in the vector pCR-Blunt II-TOPO. The resulting cDNA was employed as a template to make two different fragments of PSA by PCR with two sets of primers (SEQ ID NO: 609 and 610; and SEQ ID NO: 611 and 612). The PCR products having the expected size were used as templates to make truncated forms of PSA by PCR with the primers of SEQ ID NO: 611 and 613, which generated PSA (delta 208-218 in amino acids). The cDNA for the mature form of P703P with a 6X histidine tag at the 5' end, was prepared by PCR with P703P and the primers of SEQ ID NO: 614 and 615. The cDNA for the fusion of P703P with the truncated form of PSA (referred to as FOPP) was then obtained by PCR using the modified P703P cDNA and the truncated form of PSA cDNA as templates and the primers of SEQ ID NO: 614 and 615. The FOPP

cDNA was cloned into the NdeI site and XhoI site of the expression vector pCRX1, and confirmed by DNA sequencing. The determined cDNA sequence for the fusion construct FOPP is provided in SEQ ID NO: 616, with the amino acid sequence being provided in SEQ ID NO: 617.

5 The fusion FOPP was expressed as a single recombinant protein in *E. coli* as follows. The expression plasmid pCRX1FOPP was transformed into the *E. coli* strain BL21-CodonPlus RIL. The transformant was shown to express FOPP protein upon induction with 1 mM IPTG. The culture of the corresponding expression clone was inoculated into 25 ml LB broth containing 50 ug/ml kanamycin and 34 ug/ml
10 chloramphenicol, grown at 37 °C to OD600 of about 1, and stored at 4 °C overnight. The culture was diluted into 1 liter of TB LB containing 50 ug/ml kanamycin and 34 ug/ml chloramphenicol, and grown at 37 °C to OD600 of 0.4. IPTG was added to a final concentration of 1 mM, and the culture was incubated at 30 °C for 3 hours. The cells were pelleted by centrifugation at 5,000 RPM for 8 min. To purify the protein, the
15 cell pellet was suspended in 25 ml of 10 mM Tris-Cl pH 8.0, 2mM PMSF, complete protease inhibitor and 15 ug lysozyme. The cells were lysed at 4 °C for 30 minutes, sonicated several times and the lysate centrifuged for 30 minutes at 10,000 x g. The precipitate, which contained the inclusion body, was washed twice with 10 mM Tris-Cl pH 8.0 and 1% CHAPS. The inclusion body was dissolved in 40 ml of 10 mM Tris-Cl
20 pH 8.0, 100 mM sodium phosphate and 8 M urea. The solution was bound to 8 ml Ni-NTA (Qiagen) for one hour at room temperature. The mixture was poured into a 25 ml column and washed with 50 ml of 10 mM Tris-Cl pH 6.3, 100 mM sodium phosphate, 0.5% DOC and 8M urea. The bound protein was eluted with 350 mM imidazole, 10 mM Tris-Cl pH 8.0, 100 mM sodium phosphate and 8 M urea. The fractions containing
25 FOPP proteins were combined and dialyzed extensively against 10 mM Tris-Cl pH 4.6, aliquoted and stored at - 70 °C.

EXAMPLE 22

REAL-TIME PCR CHARACTERIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S IN
PERIPHERAL BLOOD OF PROSTATE CANCER PATIENTS

5 Circulating epithelial cells were isolated from fresh blood of normal individuals and metastatic prostate cancer patients, mRNA isolated and cDNA prepared using real-time PCR procedures. Real-time PCR was performed with the TaqmanTM procedure using both gene specific primers and probes to determine the levels of gene expression.

10 Epithelial cells were enriched from blood samples using an immunomagnetic bead separation method (DynaL A.S., Oslo, Norway). Isolated cells were lysed and the magnetic beads removed. The lysate was then processed for poly A+ mRNA isolation using magnetic beads coated with Oligo(dT)25. After washing the beads in buffer, bead/poly A+ RNA samples were suspended in 10 mM Tris HCl pH 8.0
15 and subjected to reversed transcription. The resulting cDNA was subjected to real-time PCR using gene specific primers. Beta-actin content was also determined and used for normalization. Samples with P501S copies greater than the mean of the normal samples + 3 standard deviations were considered positive. Real time PCR on blood samples was performed using the TaqmanTM procedure but extending to 50 cycles using
20 forward and reverse primers and probes specific for P501S. Of the eight samples tested, 6 were positive for P501S and β -actin signal. The remaining 2 samples had no detectable β -actin or P501S. No P501S signal was observed in the four normal blood samples tested.

EXAMPLE 23

EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGENS P703P AND P501S IN
SCID MOUSE-PASSAGED PROSTATE TUMORS

25 When considering the effectiveness of antigens in the treatment of
30 prostate cancer, the continued presence of the antigens in tumors during androgen

ablation therapy is important. The presence of the prostate-specific antigens P703P and P501S in prostate tumor samples grown in SCID mice in the presence of testosterone was evaluated as follows.

Two prostate tumors that had metastasized to the bone were removed
5 from patients, implanted into SCID mice and grown in the presence of testosterone. Tumors were evaluated for mRNA expression of P703P, P501S and PSA using quantitative real time PCR with the SYBR green assay method. Expression of P703P and P501S in a prostate tumor was used as a positive control and the absence in normal intestine and normal heart as negative controls. In both cases, the specific mRNA was
10 present in late passage tumors. Since the bone metastases were grown in the presence of testosterone, this implies that the presence of these genes would not be lost during androgen ablation therapy.

EXAMPLE 24

15 ANTI-P503S MONOCLONAL ANTIBODY INHIBITS TUMOR GROWTH *IN VIVO*

The ability of the anti-P503S monoclonal antibody 20D4 to suppress tumor formation in mice was examined as follows.

Ten SCID mice were injected subcutaneously with HEK293 cells that expressed P503S. Five mice received 150 micrograms of 20D4 intravenously at day 0
20 (time of tumor cell injection), day 5 and day 9. Tumor size was measured for 50 days. Of the five animals that received no 20D4, three formed detectable tumors after about 2 weeks which continued to enlarge throughout the study. In contrast, none of the five mice that received 20D4 formed tumors. These results demonstrate that the anti-P503S Mab 20D4 displays potent anti-tumor activity *in vivo*.

25

EXAMPLE 25

CHARACTERIZATION OF A T CELL RECEPTOR CLONE FROM A P501S-SPECIFIC T CELL CLONE

30 T cells have a limited lifespan. However, cloning of T cell receptor (TCR) chains and subsequent transfer essentially enables infinite propagation of the T

cell specificity. Cloning of tumor-antigen TCR chains allows the transfer of the specificity into T cells isolated from patients that share the TCR MHC-restricting allele. Such T cells could then be expanded and used in adoptive transfer settings to introduce the tumor antigen specificity into patients carrying tumors that express the antigen. T cell receptor alpha and beta chains from a CD8 T cell clone specific for the prostate-specific antigen P501S were isolated and sequenced as follows.

Total mRNA from 2×10^6 cells from CTL clone 4E5 (described above in Example 12) was isolated using Trizol reagent and cDNA was synthesized. To determine Va and Vb sequences in this clone, a panel of Va and Vb subtype-specific primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of the clones expressed a common Vb sequence that corresponded to the Vb7 subfamily. Furthermore, using cDNA generated from the clone, the Va sequence expressed was determined to be Va6. To clone the full TCR alpha and beta chains from clone 4E5, primers were designed that spanned the initiator and terminator-coding TCR nucleotides. The primers were as follows: TCR Valpha-6 5'(sense): GGATCC---GCCGCCACC---ATGTCACCTTTCTAGCCTGCT (SEQ ID NO: 899) BamHI site Kozak TCR alpha sequence TCR alpha 3' (antisense): GTCGAC---TCAGCTGGACCACAGCCGCAG (SEQ ID NO: 900) Sall site TCR alpha constant sequence TCR Vbeta-7. 5'(sense): GGATCC---GCCGCCACC---ATGGGCTGCAGGCTGCTCT (SEQ ID NO: 901) BamHI site Kozak TCR alpha sequence TCR beta 3' (antisense): GTCGAC---TCAGAAATCCTTTCTCTTGAC (SEQ ID NO: 902) Sall site TCR beta constant sequence. Standard 35 cycle RT-PCR reactions were established using cDNA synthesized from the CTL clone and the above primers, employing the proofreading thermostable polymerase PWO (Roche, Nutley, NJ).

The resultant specific bands (approx. 850 bp for alpha and approx. 950 for beta) were ligated into the PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E. coli* transformed with plasmids containing full-length alpha and beta chains were identified, and large scale preparations of the corresponding plasmids were generated. Plasmids containing full-length TCR alpha and beta chains were submitted

for sequencing. The sequencing reactions demonstrated the cloning of full-length TCR alpha and beta chains with the determined cDNA sequences for the Vb and Va chains being shown in SEQ ID NO: 903 and 904, respectively. The corresponding amino acid sequences are shown in SEQ ID NO: 905 and 906, respectively. The Va sequence was shown by nucleotide sequence alignment to be 99% identical (347/348) to Va6.2, and the Vb to be 99% identical to Vb7 (336/338).

EXAMPLE 26

CAPTURE OF PROSTATE SPECIFIC CELLS USING THE PROSTATE ANTIGEN P503S

10

As described above, P503S is found on the surface of prostate cells. Secondary coated microsphere beads specific for mouse IgG were coupled with the purified P503S-specific monoclonal antibody 1D12. The bound P503S antibody was then used to capture HEK cells expressing recombinant P503S. This provides a model system for prostate-specific cell capture which may be usefully employed in the detection of prostate cells in blood, and therefore in the detection of prostate cancer.

15

P503S-transfected HEK cells were harvested and redissolved in wash buffer (PBS, 0.1% BSA, 0.6% sodium citrate) at an appropriate volume to give at least 5^4 cells per sample. Round bottom Eppendorf tubes were used for all procedures involving beads. The stock concentrations were as shown below in Table VIII.

20

Table VIII

Stock concentrations	Sample concentration	Amount needed
Epithelial enrich beads 4^8 beads/ml (DynaL Biotech Inc. Lake Success, NY)	1^7 beads/ml	125 ul stock per 5 ml volume
1D12 ascites antibody 2 mg/ml	0.1 ug/ml (0.1X) to 5 ug/ml (5X) titrations	0.05 ul to 2.5 ul stock per sample
α - Mamma Mu 0.9 mg/ml	1 ug/ml (1X)	1.1 ul stock per sample
Pan-mouse IgG beads 4^8 beads/ml (DynaL Biotech)	1^7 beads/ml	125 ul stock per 5 ml volume

Blocked immunomagnetic beads were pre-washed as follows: all beads needed were pooled and washed once with 1 ml wash buffer. The beads were resuspended in a 3X volume of 1% BSA (v/v) in wash buffer and incubated for 15 min rotating at 4 °C. The beads were then washed three times with 2X volume of wash buffer and resuspended to original volume. Non-blocked beads were pooled, washed three times with 2X volume of wash buffer and resuspended to original volume.

Primary antibody was incubated with secondary beads in a fresh Eppendorf for 30 minutes, rotating at 4 °C. Approximately 200 ul wash buffer was added to increase the total volume for even mixing of the sample. The antibody-bead solution was transferred to a fresh Eppendorf, washed twice with an equal volume of wash buffer and resuspended to original volume. Target cells were added to each sample and incubated for 45 minutes, rotating at 4 °C. The tubes were transferred to a magnet, the supernatant removed, taking care not to agitate the beads, and the samples were washed twice with 1 ml wash buffer. The samples were then ready for RT-PCR using a Dynabeads mRNA direct microkit (DynaL Biotech).

Epithelial cell enrichment was placed in a magnet and supernatant was removed. The epithelial enrichment beads were then resuspended in 100 ul lysis/binding buffer fortified with Rnasin (2 U/ul per sample), and stored at -70 °C until use. Oligo (dT₂₅) Dynabeads were pre-washed as follows: all beads needed were pooled (23 ul/sample), washed three times with an excess volume of lysis/binding buffer, and resuspended to original volume. The lysis supernatant was separated with a magnet and transferred to a fresh Eppendorf. 20 ul oligo(dT₂₅) Dynabeads were added per sample and rolled for 5 min at room temperature. Supernatant was separated using a magnet and discarded, leaving the mRNA annealed to the beads. The bead/mRNA complex was washed with buffer and resuspended in cold Tris-HCl.

For RT-PCR, the Tris-HCl supernatant was separated and discarded using MPS. For each sample containing 1⁵ cells or less, the following was added to give a total volume of 30 ul: 14.25 ul H₂O; 1.5 ul BSA; 6 ul first strand buffer; 0.75 mL 10 mM dNTP mix; 3 ul Rnasin; 3 ul 0.1M dTT; and 1.5 ul Superscript II. The resulting solution was incubated for 1 hour at 42 °C, diluted 1:5 in H₂O, heated at 80°C for 2 min

to detach cDNA from the beads, and immediately placed on MPS. The supernatant containing cDNA was transferred to a new tube and stored at -20°C .

Table IX shows the percentage of capture of P503S-transfected HEK cells as determined by RT-PCR.

5

Table IX

	% capture P503S-transfected HEK cells	% capture LnCAP cells
0.1 ug/ml P503S Mab	36.90	0.00
0.5 ug/ml P503S Mab	67.40	2.93
1 ug/ml P503S Mab	40.22	0.00
5 ug/ml P503S Mab	13.11	0.00
Anti-Mu beads only, non-blocked	1.42	0.00
Anti-Mu beads only, blocked	15.65	20.21
Absolute control, non-capture cells	100.00	100.00

10

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942 under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(b) sequences having at least 70% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(c) sequences having at least 90% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(d) sequences encoded by a polynucleotide of claim 1;

(e) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and

(f) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4. A host cell transformed or transfected with an expression vector according to claim 3.

5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6. A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7. A fusion protein comprising at least one polypeptide according to claim 2.

8. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,

593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942 under moderately stringent conditions.

9. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1; and
- (c) antigen-presenting cells that express a polypeptide according to claim 2,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

10. An isolated T cell population, comprising T cells prepared according to the method of claim 9.

11. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1;
- (c) antibodies according to claim 5;
- (d) fusion proteins according to claim 7;
- (e) T cell populations according to claim 10; and
- (f) antigen presenting cells that express a polypeptide according to claim 2.

12. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 11.

13. A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 11.

14. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide according to claim 8;
- (c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and
- (d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

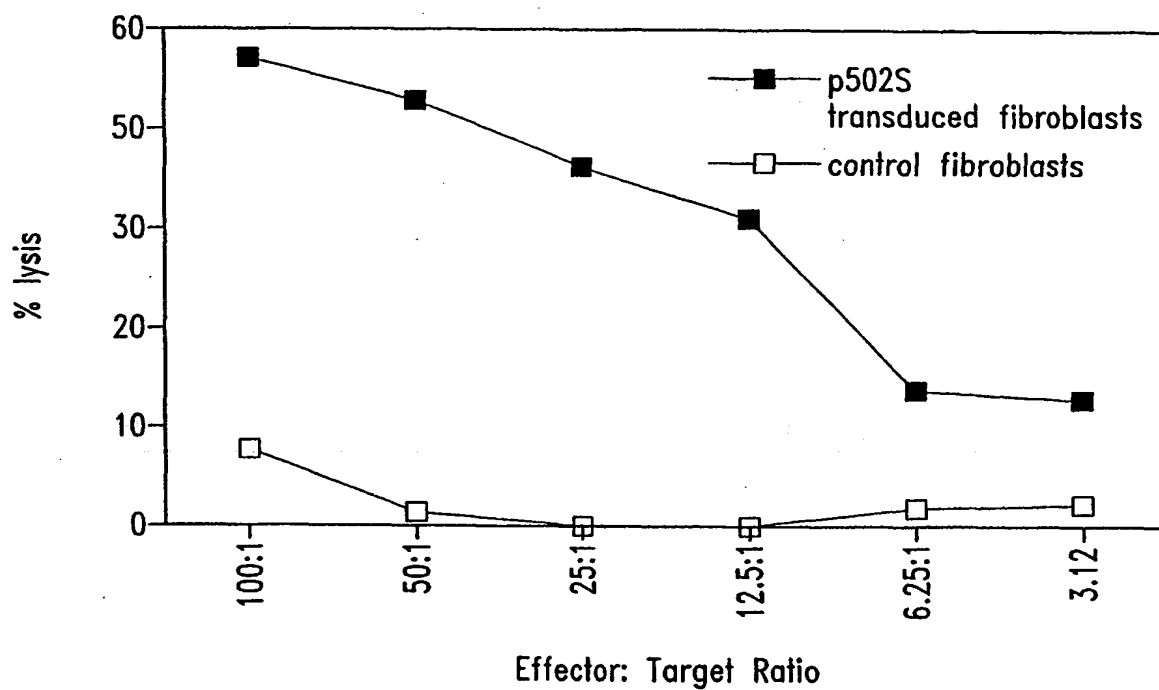
15. A diagnostic kit comprising at least one oligonucleotide according to claim 8.

16. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

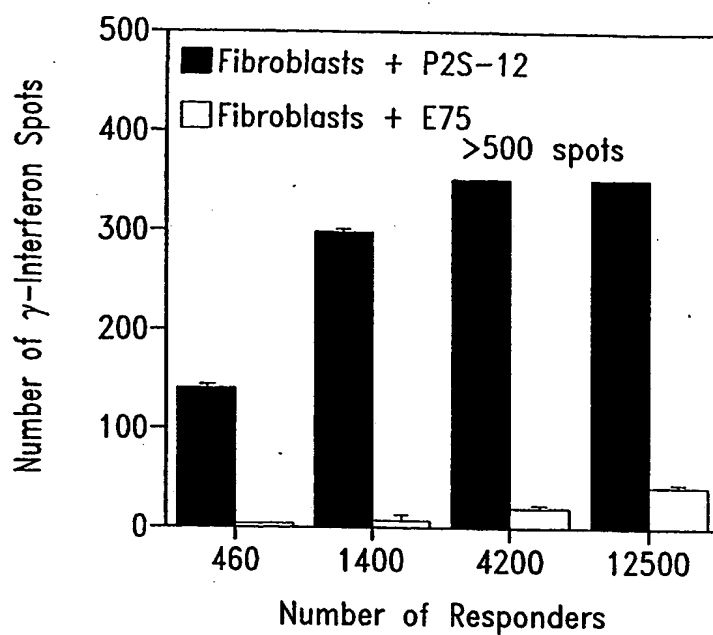
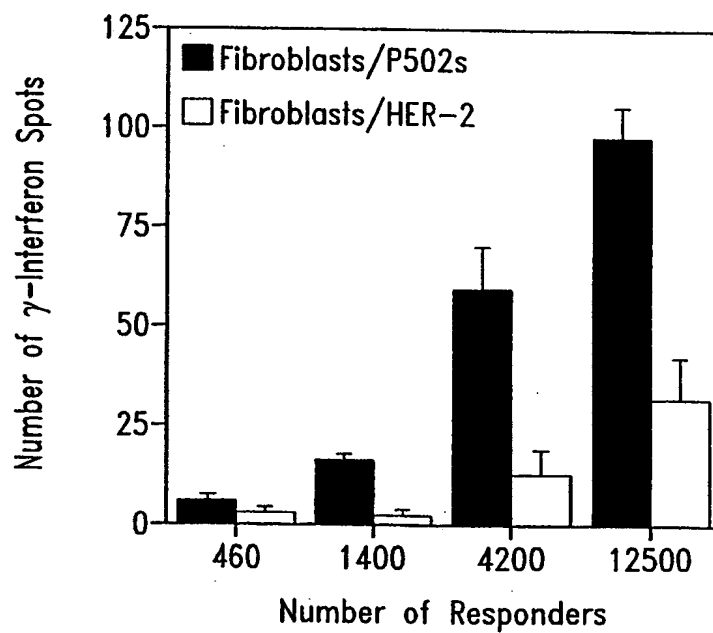
17. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

- (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate;
 - (b) administering to the patient an effective amount of the proliferated T cells,
- and thereby inhibiting the development of a cancer in the patient.

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*Fig. 1*

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*Fig. 2A**Fig. 2B*

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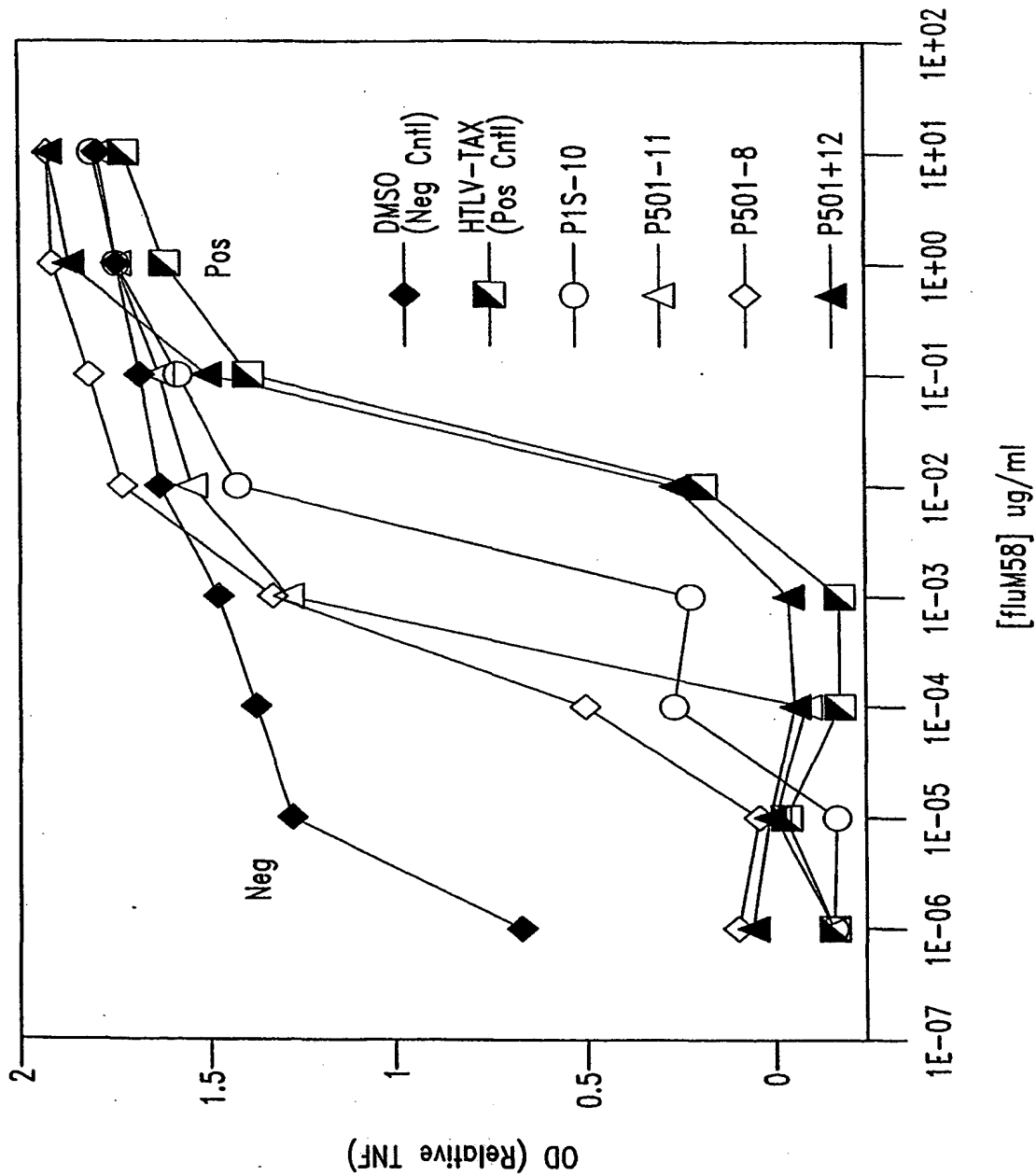
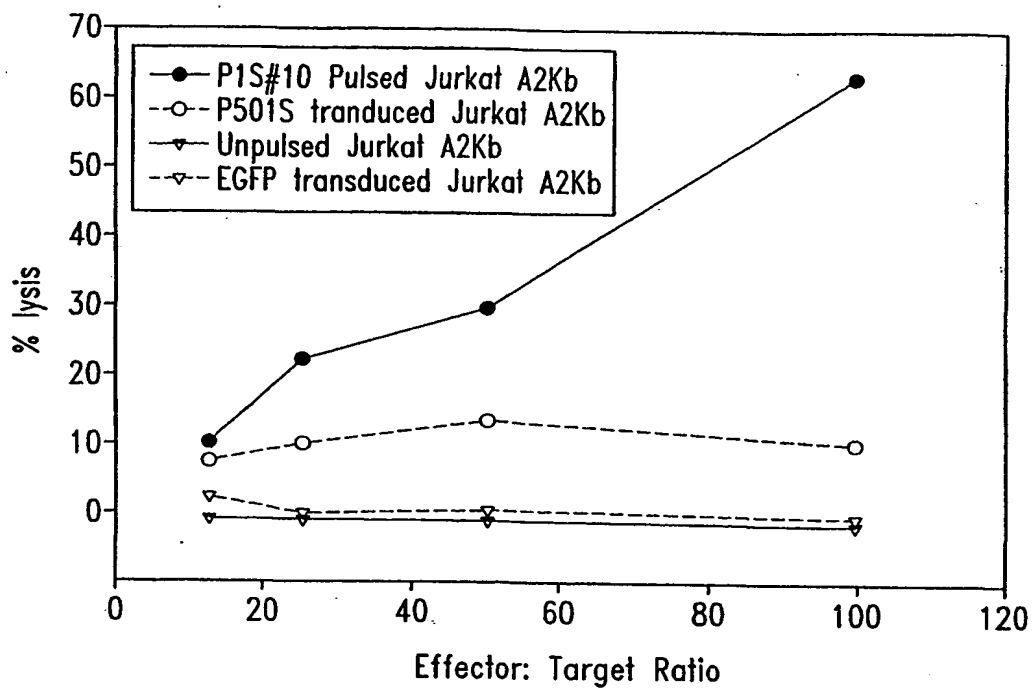
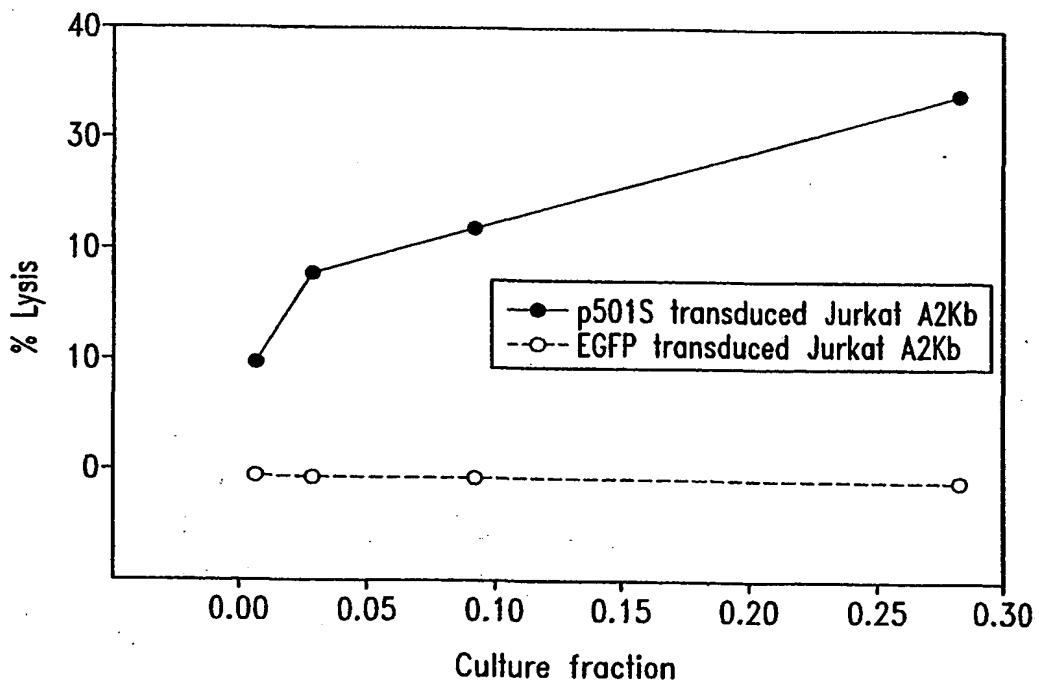
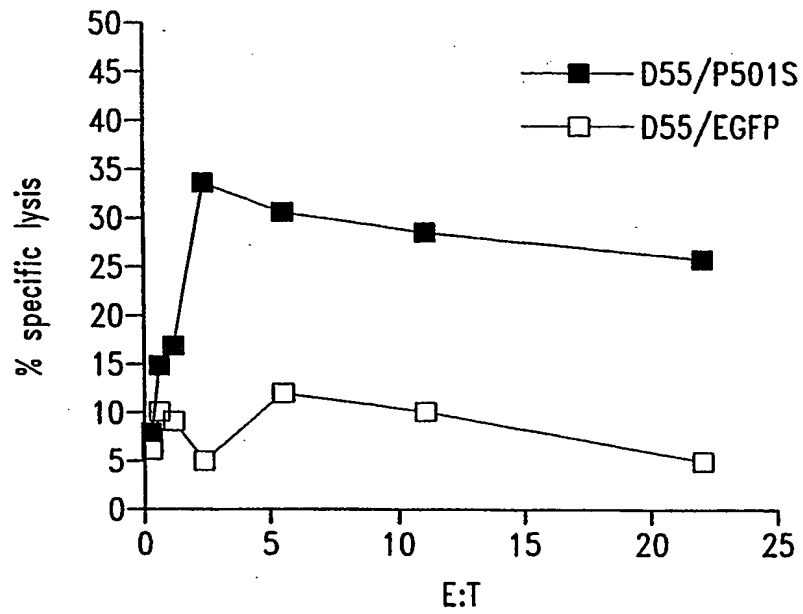
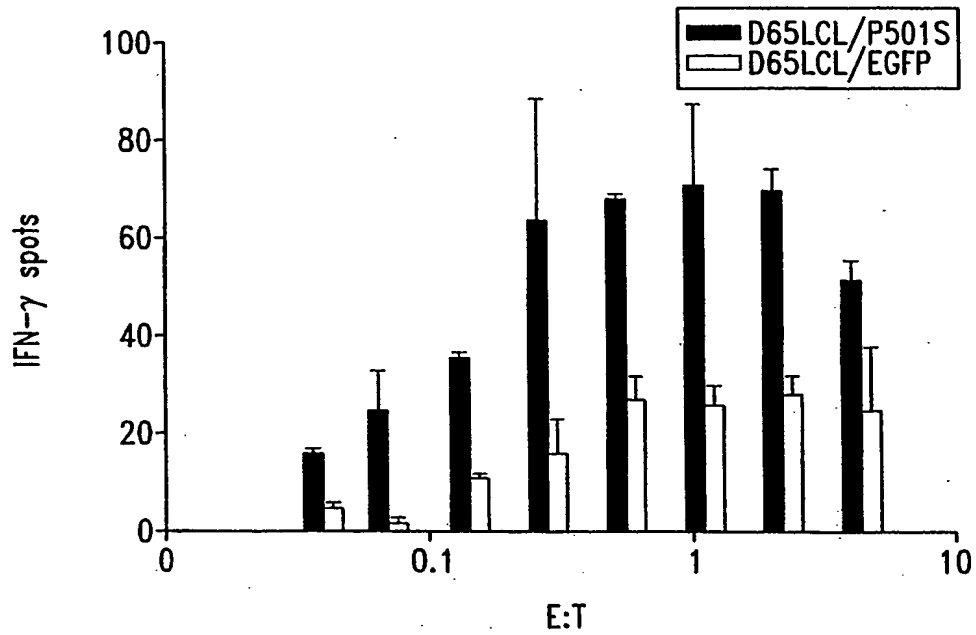


Fig. 3

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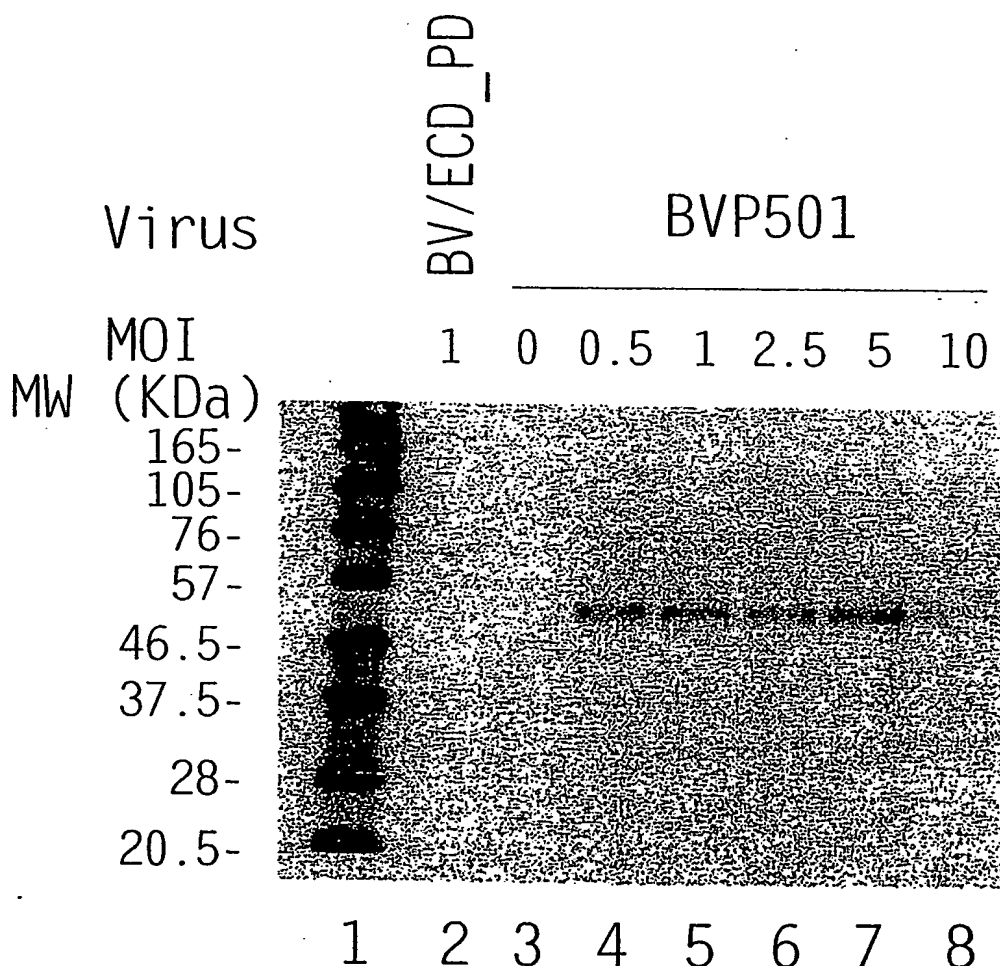
*Fig. 4**Fig. 5*

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*Fig. 6A**Fig. 6B*

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Expression of P501S
by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane2), without virus (lane3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

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FIGURE 8. Mapping of the epitope recognized by 10E3-G4-D3

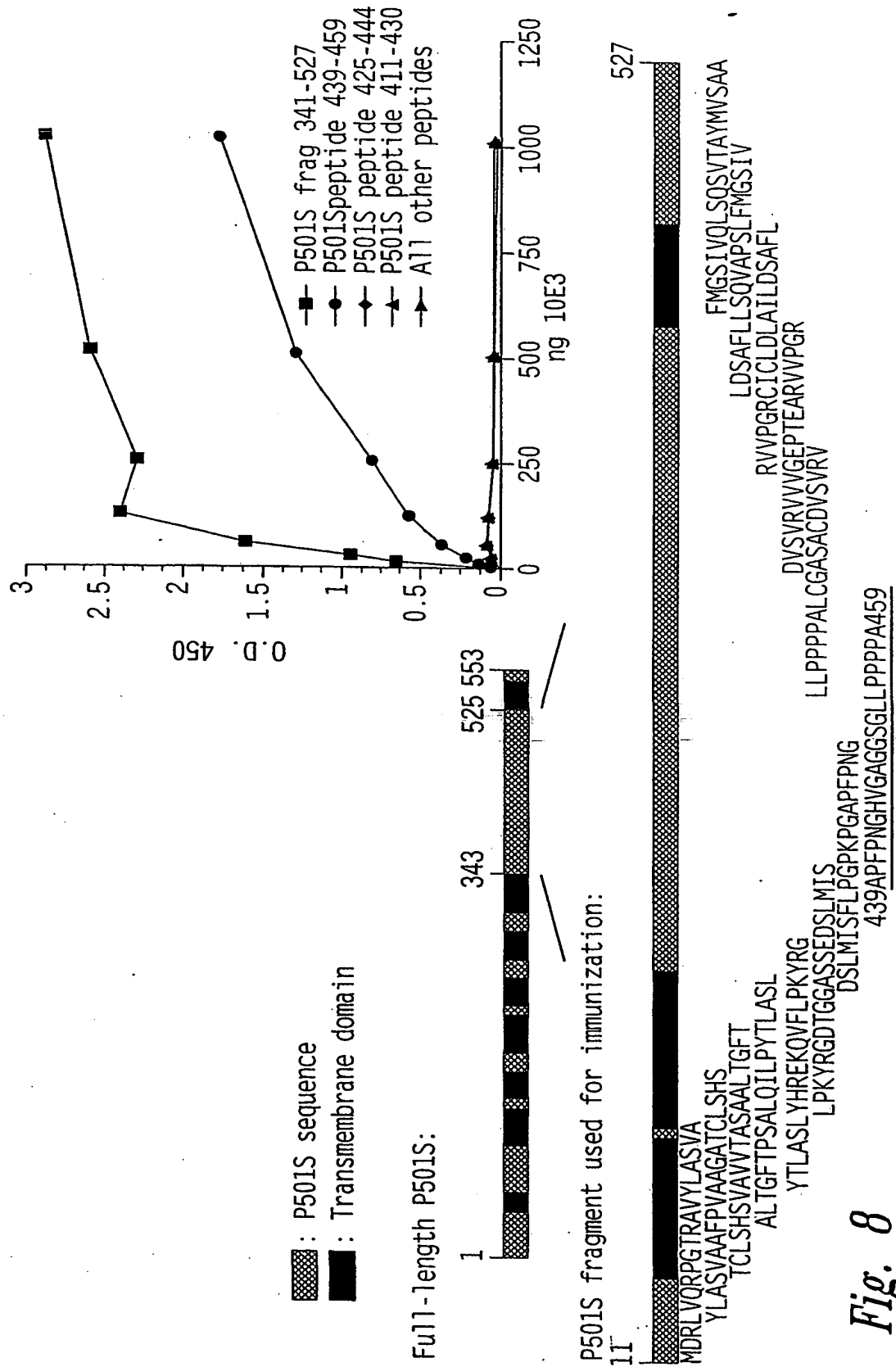


Fig. 8

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Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVLNLLTFGLEVCLAAGIT **YVPPLLLEVGVEEKFM**
TMVLGIGPVLGLVCYPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL
EALLSDLFRDPDHCRO AYSVYAFMISLGGCLGYLLPAI **DWDTSALAPYLGTEEE**

CLFGLLTILFTLCTVAATLLV AEAAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL

HQLCCRMPTLRR LFVAELCSWMALMTFTLFYTDF VGEGLYQGVPRAPGTEARRHYDEGVR

MGSLGLFLQCAISLVFSLVM DRLVQRFQTRAVYLAS VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSED* SLMTSFLPGPKPGAPFPNGHVGAGGSGL

LPPPPALCGASACDVSVRVVVGEPTARVVPGRG ICDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT *QVVFDSKDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction. J. Mol Biol. 283, 489-506.

Fig. 9

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Genomic Map of (5) Corixa Candidate Genes

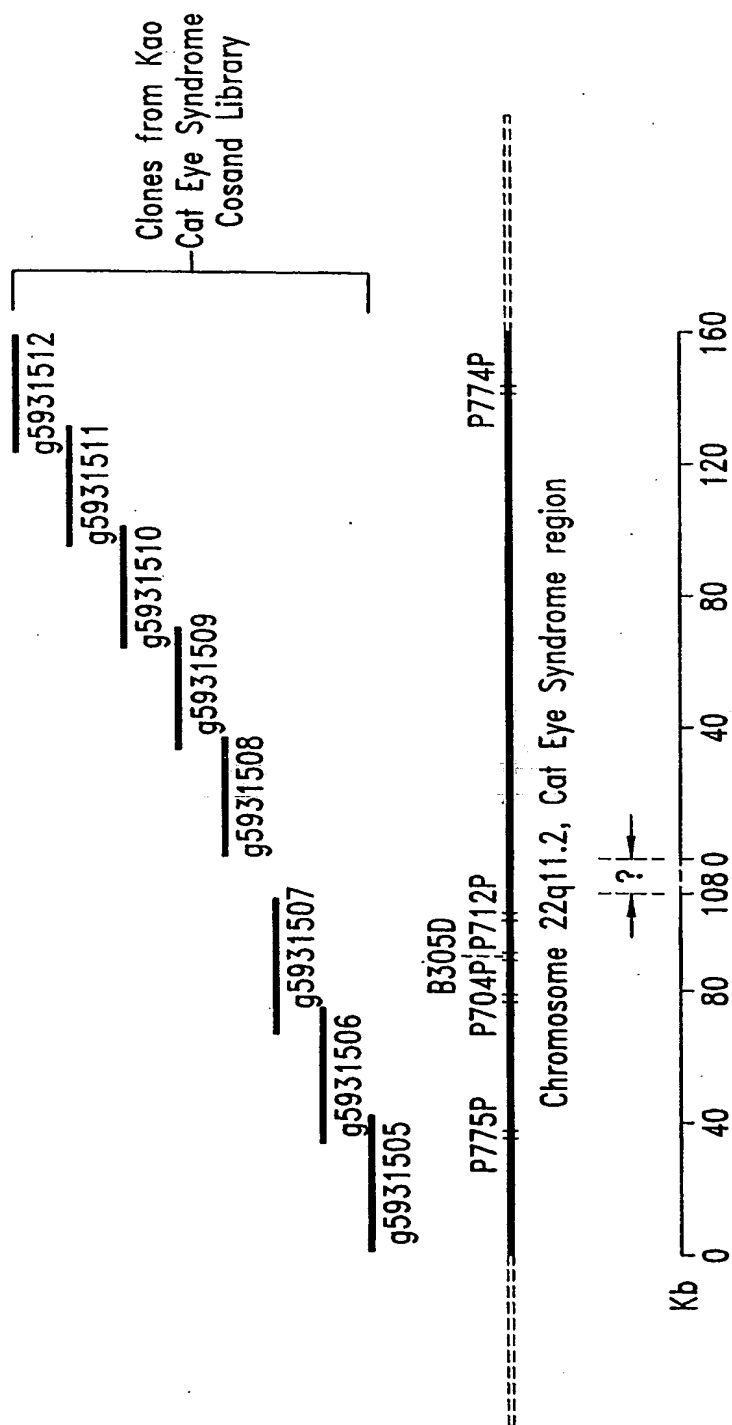


Fig. 10

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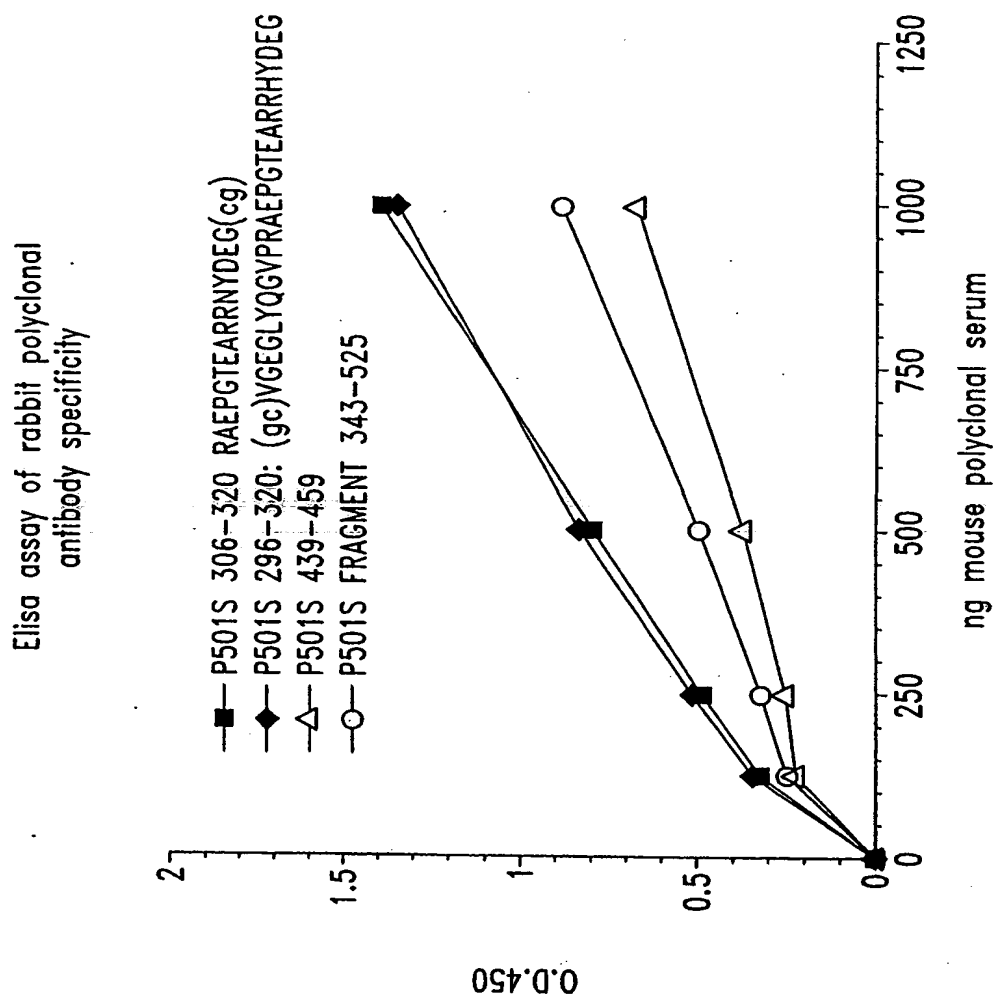


Fig. 11

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TTCTTTACCA	AAGATTCCAA	GGCCACGGAG	AATGTGTGCA	AGTGTGGCTA	TGCCCAGAGC	240
CAGCACATGG	AAGGCACCCA	GATCAACCAA	AGTGAGAAAT	GGAACACAA	GAAACACACC	300
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CACTGGCACC	TGAAAACACC	CAACCTGGTC	ATTTCTGTGA	CCGGGGGCGC	CAAGAACTTC	480
GCCCTGAAGC	CGCGCATGCG	CAAGATCTTC	AGCCGGCTCA	TCTACATCGC	GCAGTCCAAA	540
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GTGAGAGATA	ACACCATCAG	CAGGAGTTCA	GAGGAGAATA	TTGTGGCCAT	TGGCATAGCA	660
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GAGAAGCTGG	TGCGCTTTTT	ACCCCGCACG	GTGTCCCGGC	TGTCTGAGGA	GGAGACTGAG	1140
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ATGGAAGAAG	CTGGGGATGA	AATTGTGAGC	AATGCCATCT	CCTACGCTCT	ATACAAAGCC	1260
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GCTGACCTTC	AAGAAGTCAT	GTTTACGGCT	CTCATAAAGG	ACAGACCCAA	GTTTGTCCGC	1440
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CTCTTCTCCA	ACCACTTCAG	CACGCTTGTG	TACCGGAATC	TGCAGATCGC	CAAGAATTCC	1560
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CGGAAGGAAG	ACAGAAATGG	CCGGGACGAG	ATGGACATAG	AACTCCACGA	CGTGTCTCCT	1680
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AAGCTTCTGA	AGACTCTGGC	CAAAGTGAAG	AACGACATCA	ATGCTGCTGG	GGAGTCCGAG	1860
GAGCTGGCTA	ATGAGTACGA	GACCCGGGCT	GTTGAGCTGT	TCACTGAGTG	TTACAGCAGC	1920
GATGAAGACT	TGGCAGAACA	GCTGCTGGTC	TATTCCTGTG	AAGCTTGGGG	TGGAAGCAAC	1980
TGTCTGGAGC	TGGCGGTGGA	GGCCACAGAC	CAGCATTTCA	CCGCCAGCC	TGGGGTCCAG	2040
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Fig. 12A (1)

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CTGCTCATGG	ATTTCCATTC	GGTGCCACAC	CCCCCGAGC	TGGTCCTGTA	CTCGCTGGTC	2340
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CGGCTCCACT	CTTCTAATAA	AAGCTCTTTG	TATTCTGGAC	GAGTCATTTT	CTGTCTGGAC	2520
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Fig. 12A (2)

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Fig. 12A (3)

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Fig. 12B

SEQUENCE LISTING

<110> Corixa Corporation
 Xu, Jiangchun
 Dillon, Davin C.
 Mitcham, Jennifer L.
 Harlocker, Susan L.
 Yuqui, Jiang
 Kalos, Michael D.
 Fanger, Gary R.
 Retter, Marc W.
 Stolk, John A.
 Day, Craig H.
 Vedvick, Thomas S.
 Carter, Darrick
 Li, Samuel
 Wang, Aijun
 Skeiky, Yasir A.W.
 Hepler, William
 Henderson, Robert A.

<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER

<130> 210121.42723PC

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aaccacatct	acaaaatgcc	agtatcaggg	ggcggcttcg	aagccaaagt	gatgtttgga	120
tgtaaagtga	aatattagtt	ggcggatgaa	gcagatagtg	aggaaagtgt	agccaataat	180
gacgtgaagt	ccgtggaagc	ctgtggctac	aaaaaatgtt	gagccgtaga	tgccgtcgga	240
aatggtgaag	ggagactcga	agtactctga	ggctttagtg	agggtaaaat	agagacccag	300
taaaattgta	ataagcagtg	cttgaattat	ttggtttcgg	ttgttttcta	ttagactatg	360
gtgagctcag	gtgattgata	ctcctgatgc	gagtaatacg	gatgtgttta	ggagtgggac	420
ttctagggga	tttagcgggg	tgatgcctgt	tgggggccag	tgccctccta	gttggggggt	480
aggggctagg	ctggagtggt	aaaaggctca	gaaaaatcct	gcgaagaaaa	aaacttctga	540
ggtaataaat	aggattatcc	cgtatcgaag	gccttttttg	acagggtggtg	tgtggtggcc	600
ttggtatgtg	ctttctcgtg	ttacatcgcg	ccatcattgg	tatatggtta	gtgtgttggg	660
ttantangg	ctantatgaa	gaacttttgg	antggaatta	aatcaatngc	ttggccggaa	720
gtcattanga	nggctnaaaa	ggccctgtta	ngggtctggg	ctnggtttta	cccnacccat	780
ggaatncncc	ccccggacna	ntgnatccct	attcttaa			818

<210> 7
 <211> 817
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(817)
 <223> n = A,T,C or G

tttttttttt	tttttttttt	tggtctctaga	gggggtagag	ggggtgctat	agggtaaata	60
cggggccctat	ttcaaagatt	tttaggggaa	ttaattctag	gacgatgggt	atgaaactgt	120
ggtttgctcc	acagatttca	gagcattgac	cgtagtatac	ccccggtcgt	gtagcgggtga	180
aagtggtttg	gttttagacgt	ccgggaattg	catctgtttt	taagcctaata	gtggggacag	240
ctcatgagtg	caagacgtct	tgtgatgtaa	ttattatacn	aatggggggt	tcaatcgga	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggtcgcc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggt	gttctcctag	gttcaatacc	420
attggtggcc	aattgatttg	atggtaaggg	gagggatcgt	tgaactcgtc	tgttatgtaa	480
aggatncctt	ngggatggga	aggcnatnaa	ggactangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgttaat	aanaattaan	tttngttatt	600
gaatntnnng	gaaaagggtc	tacaggacta	gaaaccaaata	angaaaanta	atnntaangg	660
cnttatcntn	aaaggtnata	accnctccta	tnatcccacc	caatngnatt	ccccacncnn	720
acnattggat	nccccanttc	canaaanggc	cncccccg	tgnannccnc	cttttgttcc	780
cttnantgan	ggttattenc	ccctngcntt	atcancc			817

<210> 8
 <211> 799
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(799)
 <223> n = A,T,C or G

catttccggg	tttactttct	aaggaaagcc	gagcgggaagc	tgctaacgtg	ggaatcgggtg	60
cataaggaga	actttctgct	ggcacgcgct	agggacaagc	gggagagcga	ctccgagcgt	120
ctgaagcgca	cgtcccagaa	ggtggacttg	gcactgaaac	agctgggaca	catccgcgag	180
tacgaacagc	gcctgaaagt	gctggagcgg	gaggtccacc	agtgtagccg	cgtcctgggg	240
tgggtggcgg	angcctganc	cgctctgcct	tgctgccecc	angtgggccc	ccacccctg	300
acctgcctgg	gtccaaacac	tgagccctgc	tggcggactt	caagganaac	ccccacangg	360

5

ggattttgct	cctanantaa	ggctcatctg	ggcctcggcc	ccccacctg	gttggccttg	420
tctttgangt	gagcccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttacaa	ccacannatg	cccggctcct	cccggaaacc	antcccancc	tgnaaaggat	540
caagnccctgn	atccactnnt	nctanaaccg	gccnccnccg	cngtggaacc	cnccttntgt	600
tccttttctnt	tnagggttaa	tnncgccttg	gccttnccan	ngtcctncnc	nttttccnnt	660
gttnaaattg	ttangcnccc	nccnntcccn	cnnnncnnan	cccgaaccnn	annttnnann	720
ncctgggggt	nccnncgat	tgaccnnc	nccctntant	tgcnttnggg	nncnntgccc	780
ctttccctct	nggganncg					799

<210> 9
 <211> 801
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(801)
 <223> n = A,T,C or G

<400> 9						
acgccttgat	cctcccaggc	tgggactggt	tctggggagga	gccgggcatg	ctgtgggtttg	60
taangatgac	actcccaaag	gtggctcctga	cagtggccca	gatggacatg	gggctcacct	120
caaggacaag	gccaccagggt	gcggggggccg	aagccacat	gatccttact	ctatgagcaa	180
aatcccctgt	gggggcttct	ccttgaagtc	cgccancagg	gctcagtctt	tggacccang	240
cagggtcatgg	ggttgtngnc	caactggggg	ccncaacgca	aaanggcnc	gggcctcngn	300
cacccatccc	angacgcggc	tacactnctg	gacctccnc	tccaccactt	tcatgcgctg	360
ttentaccog	cgnatntgtc	ccanctgttt	cngtgccnac	tccancttct	nggacgtgcg	420
ctacatacgc	ccggantcnc	netcccgett	tgccctatc	caagtnccan	caacaaattt	480
cncctantg	caccnattcc	cacnttttnc	agntttccnc	nncngcttc	cttntaaaag	540
ggttgancce	cggaaaatnc	cccaaagggg	gggggccngg	tacccaactn	ccccctnata	600
gctgaantcc	ccatnaccnn	gnctcnatgg	ancntccnt	tttaannacn	ttctnaactt	660
gggaanance	ctcgnccntn	ccccnttaa	tccncccttg	cnangnncnt	ccccnntcc	720
ncccnntng	gentntnann	cnaaaaaggc	ccnnnancaa	tctcctnncn	cctcanttcg	780
ccanccctcg	aaatcggccn	c				801

<210> 10
 <211> 789
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(789)
 <223> n = A,T,C or G

<400> 10						
cagtctatnt	ggccagtgtg	gcagctttcc	ctgtggctgc	cggtgccaca	tgctgtccc	60
acagtgtggc	cgtggtgaca	gcttcagccg	ccctcaccgg	gttcaccttc	tcagccctgc	120
agatccctgcc	ctacacactg	gcctccctct	accaccggga	gaagcagggtg	ttcctgccca	180
aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	cctgatgacc	agcttccctgc	240
caggccctaa	ccctggagct	ccctcccta	atggacacgt	gggtgctgga	ggcagtggcc	300
tgctccacc	tccaccgcg	ctctgcgggg	cctctgcctg	tgatgtctcc	gtacgtgtgg	360
tggtgggtga	gccaccgan	gccagggtgg	ttccgggccg	gggcatctgc	ctggacctcg	420
ccatccctgga	tagtgcttcc	tgctgtccca	ngtggcccca	tccctgttta	tgggtcccat	480
tgtccagctc	agccagtctg	tactgccta	tatggtgtct	gccgcaggcc	tgggtctggg	540
ccatttact	ttgctacaca	ggtantattt	gacaagaacg	anttggccaa	atactcagcg	600
ttaaaaaatt	cgcacaacat	tgggggtgga	aggcctgcct	cactgggtcc	aactccccgc	660
tcctgttaac	cccatggggc	tgccggcttg	gccgccaatt	tctgttgctg	ccaaantnat	720

gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng 780
 gngttccc 789

<210> 11
 <211> 772
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(772)
 <223> n = A,T,C or G

<400> 11
 cccaccctac ccaaatatta gacaccaaca cagaaaagct agcaatggat tcccttctac 60
 tttgttaaataaataagttaaatattttaa tgcctgtgtc tctgtgatgg caacagaagg 120
 accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180
 tgtgggctga ggggacctgg ttcttgtgtg ttgccctca ggactcttcc cctacaaata 240
 actttcatat gttcaaatacc catggaggag tgtttcatcc tagaaactcc catgcaagag 300
 ctacattaaa cgaagctgca ggttaagggg cttanagatg ggaaccagg tgactgagtt 360
 tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420
 ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480
 ctccctgtat aagtccagac tgaaccccc ttggaaggnc tccagtcagg cagccctana 540
 aactggggaa aaaagaaaaa gacgccccan cccccagctg tgcanctacg cacctcaaca 600
 gcacagggtg gcagcaaaaa aaccacttta ctttggcaca acaaaaaact ngggggggca 660
 accccggcac ccnangggg gttaacagga ancnggnaa cntggaacc aattnaggca 720
 ggccnccac ccnnaatntt gctgggaaat ttttctccc ctaaattntt tc 772

<210> 12
 <211> 751
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(751)
 <223> n = A,T,C or G

<400> 12
 gcccgaattc cagctgccac accaccacg gtgactgcat tagttcggat gtcatacaaa 60
 agctgattga agcaaccctc tacttttttg tctgtgacct tttgcttggg gcaggtttca 120
 ttggctgtgt tgggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180
 aagtanggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc 240
 atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca 300
 ggcactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac 360
 agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420
 acacttgctc tcagtcttan caccatanca gccntgaaa accaananca aagaccacna 480
 cncggctgc gatgaagaaa tnaccccneg ttgacaaact tgcattggcac tggganccac 540
 agtgcccnna aaaatcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg 600
 ccaacagggg ctgccccacn cncnnaacga tgancnatt gnacaagatc tncntggtct 660
 tnatnaent gaacctgcn tngtggctcc tgttcaggnc cnnngcctga cttctnaann 720
 aangaactcn gaagncccca cngganann g 751

<210> 13
 <211> 729
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(729)
 <223> n = A,T,C or G

<400> 13

gagccaggcg	tccctctgcc	tgcccactca	gtggcaacac	ccgggagctg	ttttgtcctt	60
tgtggancct	cagcagtncc	ctctttcaga	actcantgcc	aaganccctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gctcatcttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tcggggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgag	ccggcggttgt	ggtcttagct	ctagggtttcc	tgggctgcta	tgggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcaccc	tcctcctcat	cttcattgct	420
gagggttgcaa	tgctgtggtc	gccttgggtg	acaccacaat	ggctgagcac	ttcctgacgt	480
tgctggtaat	gcctgccatc	aanaaaagat	tatgggttcc	caggaanact	tactcaagt	540
gttggaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaanagtg	cctttccccc	atttctgttg	caattgacaa	660
acgtcccca	cacagccaat	tgaaaacctg	cacccaaccc	aaangggctc	ccaaccanaa	720
attnaaggg						729

<210> 14
 <211> 816
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(816)
 <223> n = A,T,C or G

<400> 14

tgctcttct	caaagttggt	cttgttgcca	taacaaccac	cataggtaaa	gcgggagcag	60
tggtcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgacagag	tcctgtgtct	120
ggcaggtcca	cgcagtgcc	tttgtcactg	gggaaatgga	tgcgctggag	ctcgtcaaag	180
ccactcgtgt	atctttcaca	ggcagcctcg	tccgacgcgt	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcggaactg	ggtgggctga	300
cangtgccag	agcacactgg	atggcgccct	tccatgnnan	gggccctgng	ggaaagtccc	360
tganccccc	anctgcctct	caaangcccc	accttgaca	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaaggtag	ttnttcttgt	tgcccaancc	anccccntaa	acaaactctt	480
gcanatctgc	tccngggggg	tcntantacc	ancgtgggaa	aagaacccca	ggcngcgaac	540
caancttggt	tgatnccgaa	gcnataatct	nctnttctgc	ttgggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtcctcntgg	ggtgnncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	cctttnaatt	cccnanctn	ccccctggtt	tgggggtttt	720
cncnctcta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaacctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15
 <211> 783
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(783)
 <223> n = A,T,C or G

<400> 15

ccaaggcctg	ggcaggcata	nacttgaagg	tacaaccca	ggaaccctg	gtgctgaagg	60
------------	------------	------------	-----------	-----------	------------	----

atgtggaaaa	cacagattgg	cgcctactgc	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtcaact	gtgctgtcca	240
ccaagcagac	agaagactac	tgcctcgcac	ccaacaangt	gggtcgcctgc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttctgt	tatggaggct	360
gcttgggcaa	caagaacaac	taccttcggg	aagaagagtg	cattctancc	tgtcnggggtg	420
tgcaaggtgg	gcctttgana	ngcanctctg	gggtcangc	gactttcccc	cagggcccct	480
ccatggaaag	gcgccatcca	ntgttctctg	gcacctgtca	gcccaccag	ttccgctgca	540
ncaatggctg	ctgcatcnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctcccaac	aaagcttccc	tgttnaaaaa	tacnccantt	ggcttttnac	aaacncccg	660
cncctccttt	ttcccnntn	aacaaagggc	nctngccttt	gaactgccc	aaccnnggaa	720
tctnccnngg	aaaaantncc	ccccctggtt	cctnnaancc	cctccnca	anctncccc	780
ccc						783

<210> 16
 <211> 801
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(801)
 <223> n = A,T,C or G

<400> 16						
gccccaatc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttggg	gcagggttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtaggggtg	agtcctcaaa	atccgtatag	ttgggtgaagc	cacagcactt	gagccctttc	240
atgggtgggtg	tccacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtca	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgctct	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngctgcca	atgaaagaaa	ntacccacgt	tgacaaactg	catggccact	ggacgacagt	540
tgccccgaan	atcttcagaa	aagggatgcc	ccatcgattg	aacacccana	tgccactgc	600
cnacagggct	gcncncncn	gaaagaatga	gccattgaag	aaggatcttc	ntggctcttaa	660
tgaactgaaa	cctgtcatgg	tggccctgt	tcagggctct	tggcagtga	ttctganaaa	720
aaggaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17
 <211> 740
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(740)
 <223> n = A,T,C or G

<400> 17						
gtgagagcca	ggcgtccctc	tgctgcccc	ctcagtgcca	acacccggga	gctgttttgt	60
cctttgtgga	gcctcagcag	ttccctcttt	cagaactcac	tgccaagagc	cctgaacagg	120
agccaccatg	cagtgtctca	gcttcattaa	gaccatgatg	atcctcttca	atttgcctcat	180
ctttctgtgt	ggtgcagccc	tggtggcagt	gggcatctgg	gtgtcaatcg	atggggcatc	240
ctttctgaag	atcttcgggc	cactgtcgtc	cagtgccatg	cagtttgta	acgtgggcta	300
cttctctatc	gcagccggcg	ttgtgggtct	tgctcttggg	ttcctgggct	gctatgggtc	360
taagacggag	agcaagtgtg	ccctcgtgac	gttcttcttc	atcctcctcc	tcactctcat	420

tgctgaagtt	gcagctgctg	tggtcgccct	ggtgtacacc	acaatggctg	aaccattcct	480
gacgttgctg	gtantgcctg	ccatcaanaa	agattatggg	ttcccaggaa	aaattcactc	540
aantntggaa	caccnccatg	aaaagggctc	caattttctg	tggttcccc	aactataccg	600
gaattttgaa	agantcnccc	tacttccaaa	aaaaaanant	tgcttttnc	ccntttctgt	660
tgcaatgaaa	acntcccaan	acngccaatn	aaaacctgcc	cnnncaaaaa	ggntcncaaa	720
caaaaaant	nnaagggttn					740

<210> 18
 <211> 802
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(802)
 <223> n = A,T,C or G

<400> 18						
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caaggtcttc	cagctgccgc	acattacgca	gggcaagagc	ctccagcaac	actgcatatg	120
ggatacactt	tacttttagca	gccaggggtga	caactgagag	gtgtogaagc	ttattcttct	180
gagcctctgt	tagtgaggga	agattccggg	cttcagctaa	gtagtcagcg	tatgtcccat	240
aagcaaacac	tgtgagcagc	cgggaaggtag	aggcaaagtc	actctcagcc	agctctctaa	300
cattgggcat	gtccagcagt	tctccaaaca	cgtagacacc	agnngccctc	agcacctgat	360
ggatgagtgt	ggccagcgct	gcccccttgg	ccgacttggc	taggagcaga	aattgctcct	420
ggttctgccc	tgtcaccttc	acttcgcgac	tcactactgc	actgagtgtg	ggggacttgg	480
gctcaggatg	tccagagacg	tggttccgcc	ccctcnctta	atgacaccgn	ccanncaacc	540
gtcggctccc	gccgantgng	ttcgtcgtnc	ctgggtcagg	gtctgctggc	cnctacttgc	600
aancttcgtc	nggcccattg	aattcacccn	accggaactn	gtangatcca	ctnnttctat	660
aaccggnogc	caccgcnnnt	ggaactccac	tctnttntcc	tttacttgag	ggttaaggtc	720
acccttnncc	ttaccttggt	ccaaaccntn	ccntgtgtcg	anatngtnaa	tcnggnccna	780
tnccanccnc	atangaagcc	ng				802

<210> 19
 <211> 731
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(731)
 <223> n = A,T,C or G

<400> 19						
cnaagcttcc	aggtnacggg	ccgcnaance	tgaccnagg	tancanaang	cagnncgcgg	60
gagcccaccg	tcacngngng	gngtctttat	nggagggggc	ggagccacat	cnctggacnt	120
cntgacccca	actcccncc	ncncantgca	gtgatgagtg	cagaactgaa	ggtnacgtgg	180
caggaaccaa	gancaaannc	tgctccnntc	caagtccgcn	nagggggcgg	ggctggccac	240
gcncatccnt	cnagtgtctg	aaagcccnnc	cctgtctact	tgtttgagga	acngcnnga	300
catgcccagn	gttanataac	nggcngagag	tnantttgcc	tctcccttcc	ggctgcgcgn	360
cgngtntgct	tagnggacat	aacctgacta	cttaactgaa	cccnngaata	tnccnccct	420
ccactaagct	cagaacaaaa	aacttcgaca	ccactcantt	gtcacctgnc	tgctcaagta	480
aagtgtaccc	catncccaat	gtntgctnga	ngctctgncc	tgcnttangt	tcggctctgg	540
gaagacctat	caattnaagc	tatgtttctg	actgcctctt	gctccctgna	acaancnacc	600
cnnnnttcca	agggggggnc	ggcccccaat	ccccccaacc	ntnaattnan	tttancccn	660
ccccnggcc	cggcctttta	cnancntcnn	nnacngggna	aaaccnnngc	tttncccaac	720
nnaatccncc	t					731

10

<210> 20
 <211> 754
 <212> DNA
 <213> Homo sapien.

<220>
 <221> misc_feature
 <222> (1)...(754)
 <223> n = A,T,C or G

<400> 20
 tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60
 caacccccctc ntccaaatnn cnttttccgg gnggggggttc caaacccaan ttanntttgg 120
 annttaaatt aaatnttntt tggnggnnna anccnaatgt nangaaagtt naaccanta 180
 tnanccttnaa tncctggaaa ccngtngntt ccaaaaatnt ttaaccctta antccctcgg 240
 aaatngttna nggaaaaccc aanttctcnt aagggttgtt gaaggntnaa tnaaaanccc 300
 nnccaattgt ttttngccac gcctgaatta attggnntcc gntgttttcc nttaaaanaa 360
 ggnnancccc ggttantnaa tccccccnnc cccaattata ccganttttt ttngaattgg 420
 gancccnccg gaattaacgg ggnnnnntccc tnttgggggg cnggnncccc cccntcggg 480
 ggttngggnc aggnccnaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc 540
 ccaggntgag nntnggggtt ncccccccc cangggccct ctcgnanagt tgggggtttg 600
 ggggcctggg attttntttt cccnttttnc tcccccccc ccnggganag aggttngnt 660
 tttgntcncn ggccccnccn aaganctttt ccganttnan ttaaactcnt gcctnggcga 720
 agtcnttgn agggntaaan ggccccctnn cggg 754

<210> 21
 <211> 755
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(755)
 <223> n = A,T,C or G

<400> 21
 atcancccat gaccccnac nngggaccnc tcanccggnc nnncnaccnc cggccnatca 60
 nngtnagnnc actncnnttn natcacnccc cncnactac gcccncnanc cnaagcncta 120
 nncanattnc actganngcg cganngtngan ngagaaanct nataccanag ncaccanacn 180
 ccagctgtcc nanaangcct nnnatacnng nnnatccaat ntgnancctc cnaagtattn 240
 nncnncanat gattttcctn anccgattac ccntncccc tanccctc ccccaacna 300
 cgaaggcnct ggncnaagg nngcgncc cgcgtagntc ccnncaagt cncncncta 360
 aactcanccn nattacnccg ttontgagta tactccccg aatctcacc tactcaactc 420
 aaaaaanacn gatacaaat aatncaagcc tgnattatnac actntgactg ggtctctatt 480
 ttagnggtcc ntnaancntc ctaatacttc cagtctncc tcnccaattt ccnaangget 540
 ctttcngaca gcatntttt gttcccnntt gggttcttan ngaattgcc ttcntngaac 600
 gggctcntct tttcctcgg ttancctggn ttcnccggc cagttattat ttccntttt 660
 aaattcntnc cntttanttt tggcnttca aacccccggc cttgaaaacg gccccctggt 720
 aaaaggttgt tttganaaaa tttttgtttt gttcc 755

<210> 22
 <211> 849
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(849)

<223> n = A,T,C or G

<400> 22

tttttttttt	tttttangtg	tngtcgtgca	ggtagaggct	tactacaant	gtgaanacgt	60
acgctnggan	taangcgacc	cgantttctag	gannncct	aaaatcanac	tgtgaagatn	120
atcctgnnna	cggaanggtc	accggngat	nntgctagg	tgncnctcc	cannncnttn	180
cataactcng	nggccctgcc	caccaccttc	ggcgcccgng	ngnccgggcc	cggggtcattn	240
gnnttaaccn	cactnngcna	ncgggttccn	ccccnncng	accnnggga	tccgggtgnc	300
tctgtcttcc	cctgnagncn	anaaantggg	ccnccgnc	ctttaccct	nnacaagcca	360
cngccnteta	nccnccgccc	ccccccant	nngggggact	gccnanngt	ccgttntctng	420
nnaccccnnn	gggtncctcg	gttgctcgant	cnaccgnang	ccanggatc	cnaaggaagg	480
tgcgttnttg	gcccctaccc	tgcgtncgg	nncacccttc	ccgacnanga	nccgtccccg	540
cnennccngg	cctcncctcg	caacacccgc	netcntcngt	ncggnncc	ccccacccgc	600
ncectcnc	ngnccnancn	ctcncnc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccacn	ggnngacnng	nagcncntc	gcncgcgcn	gcncncct	cgcncngaa	720
ctnctcngg	ccantnncgc	tcaancnna	cnaaacgcg	ctgcgcggcc	cgnagcgncc	780
ncctcncga	gtcctcccg	cttcnacc	angnttccn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

gcgcaaacta	tacttcgtc	gnactcgtgc	gcctcgtcnc	tcttttcctc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatacn	aagntcganc	agtccaaaact	gantaacaca	120
cacacnncn	aganaaatcc	netgccttc	anagtanacn	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcga	atntgtcnc	gtttattntn	ccagntcnc	240
ctnccnacc	tacntcttcn	nagctgtcnn	acccctngtn	cgnaccccc	naggtcgga	300
tgcggtttn	nntgaccgng	cncccttc	ccccctcat	nacganccnc	ccgcaccacc	360
nanngcncgc	cccccgnnct	cttcgcnc	ctgtcctntn	ccctgtngc	ctggcnngn	420
accgcattga	ccctgcgcnn	ctncnngaaa	ncgnanacgt	ccgggttggn	annancgctg	480
tgggnngcg	tctgcncgc	gttccttcn	ncncttcca	ccatcttnt	taenggtct	540
ccnccgntc	tcnnncaac	cctgggacgc	tntcctntgc	cccccttnac	tccccctt	600
cgnccgtgnc	cgnccccacc	ntcatttnca	nacgntcttc	acaannncct	ggntnnctcc	660
cnancngncn	gtcanccnag	ggaagggngg	ggnnccnntg	nttgacgttg	nggngangtc	720
cgaanantcc	tcnccntcan	cctacccct	cgggcggnct	ctcngttnc	aacttancaa	780
ntctcccccg	ngngcncntc	tcagcctcnc	ccncccnct	ctctgcantg	tnctctgctc	840
tnaccnntac	gantnttcgn	cncctcttt	cc			872

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(815)

<223> n = A,T,C or G

<400> 24

gcatgcaagc	ttgagtattc	tatagngtca	cctaaatanc	ttggcntaat	catggtcnta	60
------------	------------	------------	------------	------------	------------	----

nctgncttcc	tgtgtcaaat	gtatacnaaa	tanatatgaa	tctnatntga	caaganngta	120
tcntncatta	gtaacaantg	tnntgtccat	cctgtcngan	canattccca	tnnattnecn	180
cgcattcnen	gncantatn	taatngggaa	ntcnntnnn	ncaccnncat	ctatcntncc	240
gcncctgac	tggnagagat	ggatnanttc	tnntntgacc	nacatgttca	tcttggattn	300
aananceccc	cgcngnccac	cgttngnng	cnagecnntc	ccaagacctc	ctgtggagggt	360
aacctgcgtc	aganncatca	aacntgggaa	acccgcnncc	angtnnaagt	ngnnncanan	420
gatcccgtcc	aggnttnacc	atcccttcnc	agcgccccct	ttngtgcctt	anagngnagc	480
gtgtccnanc	cnetcaacat	ganacgcgcc	agnccanccg	caattnggca	caatgtcgnc	540
gaaccccccta	gggggantna	tncaaanccc	caggattgtc	cncncangaa	atcccnanc	600
ccnccctac	ccncttttg	gacngtgacc	aantcccga	gtncaggtcc	ggccngnctc	660
ccccaccggt	nnccntggg	gggtgaanct	cngnntcanc	cngncgaggn	ntcgnaagga	720
accggncctn	ggncgaanng	ancnntcnga	agngccnct	cgtataaccc	cccctcncca	780
nccnacngnt	agntcccccc	cngggtncgg	aangg			815

<210> 25

<211> 775

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(775)

<223> n = A,T,C or G

<400> 25

ccgagatgtc	tcgtccgtg	gccttagctg	tgtctgcgtc	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcattccagca	gagaatggaa	120
agtcaaattt	cctgaattgc	tatgtgtctg	ggtttcatcc	atccgacatt	gaanttgc	180
tactgaagaa	tggnagaga	attgaaaaag	tgagcattc	agacttgtct	ttcagcaagg	240
actggtcttt	ctatctcntg	tactacactg	aattcaccct	cactgaaaaa	gatgagtatg	300
cctgcccgtg	gaacctatgt	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaagcagn	cnnatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcntttta	antgatatgc	ntatacaccc	taccctttat	gncccaaat	480
tgtaggggtt	acatnantgt	tcnctnngga	catgatcttc	ctttataant	cnccnttcg	540
aattgcccgt	cnccngttn	ngaattgttc	cnaaccacg	gttggtctcc	ccaggtcncc	600
tettacggaa	ggccctgggc	cnctttncaa	ggttggggga	accnaaaatt	tcncttntgc	660
cncccncca	cnntcttgng	nnncanttt	ggaacccttc	cnattccctt	tggcctcnna	720
nccttnncta	anaaaacttn	aaancgtngc	naaanntttt	acttcccccc	ttacc	775

<210> 26

<211> 820

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(820)

<223> n = A,T,C or G

<400> 26

anattantac	agtgtaatct	tttccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanagata	ncttatanca	acagtgtttt	gaccaagagc	tgctgggcac	atttcctgca	120
gaaaagggtg	cgggtcccat	cactcctcct	ctcccatagc	catcccagag	gggtgagtag	180
ccatcangcc	ttcgggtggga	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcggggg	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgaggggt	cacactataa	acgttaacga	ccnagatnan	cacctgcttc	aagtgcaccc	360
ttcctacctg	acnaccagn	accnnaact	gcngcctggg	gacagcnctg	ggancagcta	420
acnnagcact	cacctgcccc	cccattggcg	tnccntccc	tggtcctgnc	aagggaagct	480

13

```

ccctgttgga attncgggga naccaagggga nccccctcct ccanctgtga aggaaaaaann 540
gatgggaattt tnccttccg gccnntcccc tcttcttta cagccccct nntactctc 600
tccctctntt ntctgncnc acttttnacc ccnnnatctt ccttnattga tcggannctn 660
ganattccac tnnccgctnc cntcnatcng naanacnaaa nactntctna cccnggggat 720
gggnncctcg ntcatcctct ctttttctct accnccnntt ctttgcctct ccttngatca 780
tccaaccntc gntggcctn ccccccnntt tcctttncce 820

```

```

<210> 27
<211> 818
<212> DNA
<213> Homo sapien

```

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<220>
<221> misc_feature
<222> (1)...(818)
<223> n = A,T,C or G

```

```

<400> 27
tctgggtgat ggctcttcc tcctcagggga cctctgactg ctctgggcca aagaatctct 60
tgtttcttct ccgagcccca ggcagcggtg attcagccct gcccaacctg attctgatga 120
ctgcgggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggagc 180
ctgctgagca ctccgcccc tcaccctgcc cagccctgc catgagctct gggctgggtc 240
tccgctcca gggttctgct ctccangca ngccancaag tggcgctggg ccacactggc 300
ttcttctgc cccctccctg gctctganc tctgtcttcc tgctctgtgc angcncctg 360
gatctcagtt tccctcctc anngaactct gttctgann tcttcantta actntgantt 420
tatnaccnan tggctgtnc tgtcnnactt taatgggcn gaccggctaa tccctccctc 480
nctcccttcc anttctnnna accngcttnc cntctctcc centancccg ccngggaanc 540
ctcctttgcc ctaccangg gccnnnaccg cccntnctn ggggggcnng gtnctnctc 600
ctgntnnccc cctctcctnt tncctcgtcc cncncncgcn nngcannctc ncngtcccn 660
tnnctcttct ngntctgnaa ngntcncntn tnnnnngnnc ngntnntnct tccctctcnc 720
cnnntgnang tnnntnnnc ncngncccc nnnnnnnnn nggnntnnn tctnncncg 780
ccnncccc ngnattaagg cctcctctc cggccnc 818

```

```

<210> 28
<211> 731
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(731)
<223> n = A,T,C or G

```

```

<400> 28
aggaagggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg 60
tcccaacatg anggtgnngt tctcttttga angagggttg ngtttttann ccnggtgggt 120
gattnaacc cttgttatgg agnnaaagg tttnagggat ttttcggctc ttatcagtat 180
ntanattcct gtnaatcgga aaatnatntt tcnnncggaa aatnttgctc ccatccgnaa 240
attnctcccg ggtagtgcatt nttngggggn cngccangtt tcccaggctg ctanaatcgt 300
actaaagntt naagtgggan tncaaatgaa aacctnnac agagnatccn taccgactg 360
tnnnttncct tcgcccctng actctgcng agccaatac ccnngngnat gtcnccngn 420
nnngcgnnc tgaannnnnc tcngggctnn gancatcang gggtttcgca tcaaaagcnn 480
cgtttcncat naaggaactt tngcctcat caaccnctng cctcnncca tttngccgtc 540
nggttncct acgctnntng cncctnnntn ganattttnc ccgcctnggg naancctcct 600
gnaatgggta gggnccttnt ttttnaccnn gnggtntact aatcnnctnc acgctnctt 660
tctnaccccc ccccttttt caatccanc ggcnaatggg gtctcccnng cgangggggg 720
nnnccann c 731

```

<210> 29
 <211> 822
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(822)
 <223> n = A,T,C or G

<400> 29
 actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat 60
 cgctcanacc tcacanccctc ccnacnangc ctataangaa nannaataga nctgtncnnt 120
 atntntacnc tcatanncct cnnnaccacac tccctcttaa cccntactgt gcctatngcn 180
 tnnetantct ntgccgcctn cnanccacccn gtggggccnac cncnngnatt ctcnatctcc 240
 tcnccatntn gcctananta ngtncataacc ctataccctac nccaatgcta nnnctaancn 300
 tccatnantt annntaacta ccactgaent ngactttcnc atnanctcct aatttgaatc 360
 tactctgact cccacngcct annnattagc anentcccc nacnatntct caaccaaadc 420
 ntcaacaacc tatctanctg ttcnccaacc nttnectccg atccccnnac aacccccctc 480
 ccaaataccc nccacctgac ncctaaccn caccatcccg gcaagccnan ggcatttan 540
 ccactggaat cacnatngga naaaaaaaaaa ccnaactctc tancncnnat ctccctaana 600
 aatnctctn naatttactn ncantnccat caanccccacn tgaaacnnaa cccctgtttt 660
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc cccccnctnc 720
 ccnaatgaag gncnccaat cnangaaacg nccntgaaaa ancnaaggcna anannntccg 780
 canatcctat cccttanttn ggggnccctt nccnngggcc cc 822

<210> 30
 <211> 787
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(787)
 <223> n = A,T,C or G

<400> 30
 cggccgcctg ctctggcaca tgcctcctga atggcatcaa aagtgatgga ctgcccattg 60
 ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120
 gtctgcagga ttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna 180
 gctggaagcc ctggagggcc tctctcgcca gcctccccct tctctccacg ctctccangg 240
 acaccagggg ctccaggcag cccattatcc ccagnangac atgggtgttc tccacgcgga 300
 cccatggggc ctgnaaggcc agggctctcct ttgacaccat ctctcccgtc ctgctggca 360
 ggccgtggga tccactantt ctanaacggn cgccaccncg gtgggagctc cagcttttgt 420
 tcccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt 480
 gtgaaattgt ttntccccctc ncnattccnc ncnacatacn aacccggaan cataaagtgt 540
 taaagcctgg gggtnccctn nngaataaac tnaactcaat taattgcgtt ggctcatggc 600
 ccgctttccn ttcnngaaaa ctgtcntccc ctgcnttntt gaatcgcca cccccnggg 660
 aaaagcggtt tgcnttttng ggggntcctt ccncttcccc cctcnctaan ccctnccct 720
 cggctgttnc nggtngcggg gaangggnat nnnctccnc naagggggng agnnngntat 780
 ccccaaa 787

<210> 31
 <211> 799
 <212> DNA
 <213> Homo sapien

<220>

15

<221> misc_feature
 <222> (1)...(799)
 <223> n = A,T,C or G

<400> 31
 tttttttttt tttttttggc gatgctactg ttttaattgca ggaggtgggg gtgtgtgtac 60
 catgtaccag ggctattaga agcaagaagg aaggagggag ggcagagcgc cctgctgagc 120
 aacaaaggac tcctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct 180
 cccgcagggt gggggccacc agtccagggt tgggagcact acanggggtg ggagtgggtg 240
 gtggctggtg cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca 300
 ggggaccttc tgttctccca nggnaacttc nttnatctcn aaagaacaca actgtttctt 360
 cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttgggtaca 420
 tatggttccg gccacacctc ccntcnaa aagtaattca ccccccccn ccntctnttg 480
 cctgggccct taantaccca caccggaact canttantta ttcactcttg gntgggcttg 540
 ntnatcnccn cctgaangcg ccaagttgaa aggccacgcc gtncnccnctc cccatagnan 600
 nttttnnct canctaattgc cccccnggc aacnatccaa tcccccccn tgggggcccc 660
 agcccaangc ccccgctcg ggnnncnngn cncgnantcc ccaggntctc ccantcngnc 720
 ccnnngcncc cccgcacgca gaacanaagg ntngagccnc cgcannnnnn nggtnnncac 780
 ctgccccccc cenncgngg 799

<210> 32
 <211> 789
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(789)
 <223> n = A,T,C or G

<400> 32
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
 ttttnccnag ggcagggtta ttgacaacct cncgggacac aancaggctg gggacaggac 120
 ggcaacaggc tccggcgcg ggcggcgcg ccctacctgc ggtaccaa atgtgcagcctc 180
 cgctcccgct tgatnttct ctgcagctgc aggatgccnt aaaacagggc ctcgcccntn 240
 ggtgggcacc ctgggatttn aatttcacag ggcacaatgc ggtcgcanc cctcaccacc 300
 nattaggaat agtggtnnta ccnccnccg ttggcncact cccntggaa accacttntc 360
 gcggctccgg catctggtct taaacctgc aaacnctggg gccctctttt tggttantnt 420
 nccngccaca atcatnact agactggcnc gggctggccc caaaaaancn ccccaaaacc 480
 ggnccatgtc ttncgggggt tgetgcnatn tncatcacct cccgggcnc naaggnaaac 540
 ccaaaagtgc ttgnggccn caaaaaanct ccggggggnc ccagtttcaa caaagtcac 600
 ccccttggcc cccaaatcct cccccgntt nctgggtttg ggaacccacg cctctnnctt 660
 tggnnngcaa gntgntccc ccttcgggcc cccgggtggc ccnctctaa ngaaaacncc 720
 ntcctnnnca ccattcccc nngnnacgnc tancaangna tccctttttt tanaaacggg 780
 cccccnccg 789

<210> 33
 <211> 793
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(793)
 <223> n = A,T,C or G

<400> 33
 gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg 60

aattcatggc	tgttggagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgatgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtattt	gcaaagaaga	cgaaggcaga	gtggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggttctga	cttttgagga	ggttgttcat	catgatcaca	300
acaangaacg	gggctcgttt	atcaccantg	aggagcagga	cgtgagcccc	cgccctgcac	360
ctctgctggt	aaacacccca	gccatccctt	ctttcaaaaag	ggatccacta	cttctagagc	420
ggncgccacc	gcggtggagc	tccagctttt	gttcccttta	gtgagggtta	attgcgcgct	480
tggcgtaatc	atggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaathtt	aaagcctggg	ggtngcctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgttttcc	agtccggaaa	acctgtcctt	660
gccagctgcc	nttaatgaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgcncctccc	gctttctcgc	ttcctgaant	ccttcccccc	ggtctttcgg	cttgccgcna	780
acggtatcna	cct					793

<210> 34
 <211> 756
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(756)
 <223> n = A,T,C or G

<400> 34						
gccgcgaccg	gcatgtacga	gcaactcaag	ggcgagtggga	accgtaaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagtct	ttctggagct	caacttcttg	120
ccaaccacag	ggaccaaget	gaccaaacag	cagctaattc	tggcccgtga	catactggag	180
atcggggccc	aatggagcat	cctacgcaan	gacatcccct	ccttcgagcg	ctacatggcc	240
cagctcaaat	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttcctg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tgganggcag	ctaccncaa	gtnttcctgg	ccnagggtaa	480
catccccgcg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcagggatg	540
aaaatcgcn	ggttgctcca	gaaaggctnc	aanaanatcc	ttttcnctga	aggccccggg	600
atnncntagt	nctagaatcg	gcccgccatc	gcggtgganc	ctccaacctt	tcgttnccct	660
ttactgaggg	ttnattgccg	cccttggcgt	tatcatggtc	acnccngttn	cctgtgttga	720
aattnttaac	ccccacaaat	tccaagccna	cattng			756

<210> 35
 <211> 834
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(834)
 <223> n = A,T,C or G

<400> 35						
ggggatctct	anactnacct	gnatgcattg	ttgtcgggtg	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggct	gctgtnttta	agttgctcag	tctgccgtca	120
tagtcagaca	cnctcttggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcngg	gctgtctgct	cggtgaactc	gatgacnang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctcct	tggtgacctc	cccttcaaa	ttgttccggc	cttcatcaaa	300
cttctnnaan	angannancc	canttttgtc	gagctggnat	ttgganaaca	cgctactggt	360
ggaaactgat	cccaaatggg	atgtcatcca	tcgcctctgc	tgctgcaaaa	aaacttgctt	420
ggcncaaatc	cgactcccn	tccttgaaag	aagccnatca	cacccccctc	cctggactcc	480

17

nncaangact	ctncegctnc	ccntccnng	cagggttggt	ggcannccgg	gccntgccc	540
ttcttcagcc	agttcacnat	nttcacagc	ccctctgcc	gctgtntat	tccttgggg	600
ggaanccgtc	tctcccttc	tgaannaact	ttgaccgtng	gaatagccgc	gcntcncnt	660
acntnctggg	ccgggttcaa	antccctccn	ttgncnntcn	cctcgggcca	ttctggattt	720
nccnaacttt	ttccttcccc	cncccnccgg	ngtttggnnt	tttcatnggg	ccccaaactt	780
gctnttgccc	antcccttgg	gggcntntan	cnccccctnt	ggtcccntng	ggcc	834

<210> 36
 <211> 814
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(814)
 <223> n = A,T,C or G

cggnccgttt	ccngccgcgc	cccgtttcca	tgacnaaggc	tcctttcang	ttaaatacnn	60
cctagnaaac	attaatgggt	tgctctacta	atacatcata	cnaaccagta	agcctgccc	120
naacgccaac	tcaggccatt	cctaccacaa	gaagaaaggc	tggtctctcc	acccctgtg	180
ggaaaggcct	gccttgtaag	acaccacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanagggttt	gttctcatgg	ctgcccaccg	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgtcttt	ttggacatca	360
ggcttgatgg	tatcaactgcc	acntttccac	ccagctgggc	ncccttcccc	catntttgtc	420
antganctgg	aaggcctgaa	ncttagtctc	caaaaagtctc	ngcccacaag	accggccacc	480
aggggangtc	ntttncagtg	gatctgccaa	anantaccn	tatcatcnnt	gaataaaaag	540
geccctgaac	ganatgcttc	cancancctt	taagacccat	aatcctngaa	ccatgggtgc	600
cttccgggtc	gatecnaaag	gaatgttcct	gggtcccant	ccctcctttg	ttnccttact	660
tgtnttgga	ccntgctngn	atnaccnaan	tganatcccc	ngaagcacc	tnccctggc	720
atttganttt	cntaaattct	ctgccctacn	nctgaaaagca	cnattccctn	ggcncnnaan	780
ggngaactca	agaaggctcn	ngaaaaacca	cncn			814

<210> 37
 <211> 760
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(760)
 <223> n = A,T,C or G

gcatgctgct	cttctcctaaa	gttggttcttg	ttgccataac	aaccaccata	ggtaaagcgg	60
gcgcagtggt	cgctgaagg	gttgtagtac	cagcgcgga	tgctctcctt	gcagagtcct	120
gtgtctggca	ggctccacgca	atgccctttg	tcactgggga	aatggatgcg	ctggagctcg	180
tcnaanccac	tcgtgtattt	ttcacangca	gcctcctccg	aagcntccgg	gcagttgggg	240
gtgtcgtcac	actccactaa	actgtcgatn	cancagccca	ttgctgcage	ggaactgggt	300
gggtgacag	tgccagaaac	acactggatn	ggcctttcca	tggaaaggcc	tgggggaaat	360
cncctnancc	caaactgcct	ctcaaaggcc	accttgcaca	ccccgacagg	ctagaaatgc	420
actcttcttc	ccaaaggtag	ttgttcttgt	tgcccaagca	ncctccanca	aacccaaanc	480
ttgcaaaatc	tgctccgtgg	gggtcatnnn	taccanggtt	ggggaaanaa	acccggcngn	540
ganccnccct	gtttgaatgc	naaggnaata	atcctcctgt	cttgcttggg	tggaaanagca	600
caattgaact	gttaacnttg	ggccnggttc	cnctnggggtg	gtctgaaact	aatcaccgtc	660
actggaaaaa	ggtangtgcc	ttccttgaat	tcccaaantt	cccctngntt	tgggtntttt	720
ctcctctncc	ctaaaaaatcg	tnttcccccc	ccntanggcg			760

<210> 38
 <211> 724
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(724)
 <223> n = A,T,C or G

<400> 38
 tttttttttt tttttttttt tttttttttt ttttttaaaaa cccctcccat tgaatgaaaa 60
 ctccnaaat tgtccaaccc cctennccaa atnnccattt ccgggggggg gttccaaacc 120
 caaattaatt ttgganttta aattaaatnt tnattngggg aanaanccaa atgtnaagaa 180
 aatttaaccc attatnaact taaatnccn gaaaccntg gnttccaaaa atttttaacc 240
 cttaaattcc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaagggt 300
 ngatttaaac ccccttnant tnttttnacc cnnngctnaa ntatttngnt tccggtgttt 360
 tcctnttaan cntnggtaac tcccgntaat gaannnccct aanccaatta aaccgaattt 420
 tttttgaatt ggaaattccn ngggaattna ccgggggttt tcccnttttg gggccatncc 480
 cccncttttc gggtttggn ntaggttgaa ttttttnang nccccaaaaa ncccccaana 540
 aaaaactcc caagnnttaa ttngaantnc ccccttccca ggccttttg gaaaggnggg 600
 tttntggggg ccngggantt cnttcccccn ttncncccc cccccnggt aaanggttat 660
 ngnttttggg ttttgggcc cttnanggac ctccgggatn gaaattaaat ccccggnccg 720
 gccg 724

<210> 39
 <211> 751
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(751)
 <223> n = A,T,C or G

<400> 39
 tttttttttt tttttotttg ctcacattta atttttattt tgattttttt taatgctgca 60
 caacacaata tttatttcat ttgtttcttt tatttcattt tatttggttg ctgctgctgt 120
 tttatttatt tttactgaaa gtgagaggga acttttgttg ccttttttcc tttttctgta 180
 ggccgcctta agctttctaa atttggaaca tctaagcaag ctgaanggaa aaggggggtt 240
 cgcaaatca ctgggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga 300
 ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc ttttaattana 360
 cttgggggtt cctccccan accaaccnccn ctgacaaaaa gtgccngccc tcaaatnatg 420
 tcccggcnnt cnttgaaaca cacngcngaa ngttctcatt ntccccncnc caggtnaaaa 480
 tgaagggtta ccatntttta cncacctcc acntggcnnn gcctgaatcc tcnaaaancn 540
 cctcaancn aattnctnng ccccggtcnc gcntnngtcc cncocgggt cgggaantn 600
 cccccnga anncnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc 660
 cnnagactnt cctcnncnan cncaattttc ttttnntcac gaacnccnnc cnnaaatgn 720
 nnnncnctc cncnngtcn naatcnccan c 751

<210> 40
 <211> 753
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(753)

<223> n = A,T,C or G

<400> 40

gtggtatttt	ctgtaagatc	aggtgttcct	ccctcgtagg	tttagaggaa	acaccctcat	60
agatgaaaac	ccccccgaga	cagcagcact	gcaactgcc	agcagccggg	gtaggagggg	120
cgccctatgc	acagctgggc	ccttgagaca	gcagggttc	gatgtcaggc	tcgatgtcaa	180
tggtctggaa	gcggcggtg	tacctgcgta	ggggcacacc	gtcagggccc	accaggaact	240
tctcaaagtt	ccaggcaacn	tcgttgcgac	acaccggaga	ccaggtgatn	agcttggggg	300
cggtcataan	cgcggtggcg	tcgtcgctgg	gagctggcag	ggcctcccgc	aggaaggcna	360
ataaaaggtg	cgcccccgca	ccgttcant	cgacttctc	naanaccatg	angttgggct	420
cnaaccacc	accannccgg	acttccttga	nggaattccc	aaatctcttc	gntcttgggc	480
ttctnctgat	gccctantg	gttgccnngn	atgccaanca	nccccaancc	ccgggggtcct	540
aaanaccn	cctcctcntt	tcactctggg	tnntntcccc	ggaccntggg	tcctctcaag	600
ggancccata	tctcnaccan	tactcacnt	nccccccnt	gnnaccanc	cttctanngn	660
ttccncccg	ncctctggcc	cntcaaan	gcttnacna	cctgggtctg	ccttcccccc	720
tnccctatct	gnacccn	ttgtctcan	tn			753

<210> 41

<211> 341

<212> DNA

<213> Homo sapien

<400> 41

actatatcca	tcacaacaga	catgcttcat	cccatagact	tcttgacata	gcttcaaagt	60
agtgaaccca	tccttgattt	atatacatat	atgttctcag	tattttggga	gcctttccac	120
ttctttaaac	cttgctcatt	atgaacactg	aaaataggaa	tttgtgaaga	gttaaaaagt	180
tatagcttgt	ttacgtagta	agtttttgaa	gtctacattc	aatccagaca	cttagttgag	240
tggtaaactg	tgatttttaa	aaaatatcat	ttgagaatat	tctttcagag	gtattttcat	300
ttttactttt	tgattaaattg	tgttttatat	attagggtag	t		341

<210> 42

<211> 101

<212> DNA

<213> Homo sapien

<400> 42

acttactgaa	tttagttctg	tgctcttcct	tatttagtgt	tgtatcataa	atactttgat	60
gtttcaaaca	ttctaaataa	ataattttca	gtggcttcat	a		101

<210> 43

<211> 305

<212> DNA

<213> Homo sapien

<400> 43

acatctttgt	tacagtctaa	gatgtgttct	taaatcacca	ttccttcctg	gtcctcacc	60
tccagggtgg	tctcacactg	taattagagc	tattgaggag	tctttacagc	aaattaagat	120
tcagatgcct	tgctaagtct	agagttctag	agttatgttt	cagaaagtct	aagaaaccca	180
cctcttgaga	ggtcagtaaa	gaggacttaa	tatttcatat	ctacaaaatg	accacaggat	240
tgatacaga	acgagagtta	tcttgataa	ctcagagctg	agtacctgcc	cgggggccgc	300
tcgaa						305

<210> 44

<211> 852

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(852)
 <223> n = A,T,C or G

<400> 44

acataaatat	cagagaaaag	tagtctttga	aatatttacg	tccaggagtt	ctttgtttct	60
gattatttgg	tgtgtgtttt	ggtttgtgtc	caaagtattg	gcagcttcag	ttttcatttt	120
ctctccatcc	tcgggcattc	ttcccaaatt	tatataccag	tcttcgtcca	tccacacgct	180
ccagaatttc	tctttttag	taatatctca	tagctcggct	gagcttttca	taggtcatgc	240
tgctgttgtt	cttcttttta	ccccatagct	gagccactgc	ctctgatttc	aagaacctga	300
agacgccctc	agatcgggtc	tcccatttta	ttaatcctgg	gttcttgtct	gggttcaaga	360
ggatgtcgcg	gatgaattcc	cataagttag	tccctctcgg	gttgtgcttt	ttggtgtggc	420
acttggcagg	ggggctcttc	tcctttttca	tatcaggtga	ctctgcaaca	ggaaggtgac	480
tggtggttgt	catggagatc	tgagcccggc	agaaagtttt	gctgtccaac	aaatctactg	540
tgctaccata	gttgggtgtc	tataaatagt	tctngtcttt	ccaggtgttc	atgatggaag	600
gctcagtttg	ttcagtcttg	acaatgacat	tgtgtgtgga	ctggaacagg	tcactactgc	660
actggccgtt	ccacttcaga	tgctgcaagt	tgctgtagag	gagntgcccc	gccgtccctg	720
ccgcccgggt	gaactcctgc	aaactcatgc	tgcaaagggt	ctcgccgttg	atgtcgaaact	780
cntggaaaag	gatacaattg	gcatccagct	ggttgggtgc	caggaggtga	tggagccact	840
cccacacctg	gt					852

<210> 45
 <211> 234
 <212> DNA
 <213> Homo sapien

<400> 45

acaacagacc	cttgctcgct	aacgacctca	tgctcatcaa	gttggacgaa	tccgtgtccg	60
agtctgacac	catccggagc	atcagcattg	cttgcagtg	ccctaccgcg	gggaactctt	120
gcctcgtttc	tggtctgggt	ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	180
tgaacgtgtc	ggtgggtgtc	gaggaggtct	gcagtaagct	ctatgaccgg	ctgt	234

<210> 46
 <211> 590
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(590)
 <223> n = A,T,C or G

<400> 46

actttttatt	taaatgttta	taaggcagat	ctatgagaat	gatagaaaac	atgggtgtgta	60
atttgatagc	aatatttttg	agattacaga	gttttagtaa	ttaccaatta	cacagttaaa	120
aagaagataa	tatattccaa	gcanatacaa	aatatctaata	gaaagatcaa	ggcaggaaaa	180
tgantataac	taattgacaa	tggaataatca	attttaatgt	gaattgcaca	ttatccttta	240
aaagctttca	aaanaanaaa	ttattgcagt	ctanttaatt	caaacagtgt	taaatggtat	300
caggataaan	aactgaaggg	canaaaagaat	taattttcac	ttcatgtaac	ncacccanat	360
ttacaatggc	ttaaatgcan	ggaaaaagca	gtggaagtag	ggaagtantc	aaggtctttc	420
tggtctctaa	tctgccttac	tctttgggtg	tggtcttgat	cctctggaga	cagctgccag	480
ggctcctgtt	atatccacaa	tcccagcagc	aagatgaagg	gatgaaaaag	gacacatgct	540
gccttccttt	gaggagactt	catctcactg	gccaacactc	agtcacatgt		590

<210> 47
 <211> 774
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(774)
 <223> n = A,T,C or G

<400> 47
 acaagggggc ataatgaagg agtggggana gatttttaag aaggaaaaaa aacgaggccc 60
 tgaacagaat tttcctgnac aacggggcct caaaataatt ttcttgggga gggtcaagac 120
 gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg 180
 cattacagac gggactctgg gaggaaggat aaacagaaag gggacaaagg ctaatcccaa 240
 aacatcaaag aaaggaaggt ggcgtcatal ctcccagcct acacagttct ccagggtctct 300
 cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtgt 360
 ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgtgat cctgcgtggc 420
 ccacactcct tgaacacaca tccccagggt atattcctgg acatggctga acctcctatt 480
 cctacttccg agatgccttg ctccctgcag cctgtcaaaa tccactcac cctccaaacc 540
 acggcatggg aagcctttct gacttgccctg attactccag catcttgga caatccctga 600
 ttccccactc cttagaggca agataggggtg gttaagagta gggctggacc acttgagacc 660
 aggtgctgg cttcaaattt tggctcattt acgagctatg ggaccttggg caagtnatct 720
 tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

<210> 48
 <211> 124
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(124)
 <223> n = A,T,C or G

<400> 48
 canaaattga aattttataa aaaggcattt ttctottata tccataaaat gatataattt 60
 ttgcaantat anaaatgtgt cataaattat aatgttccct aattacagct caacgcaact 120
 tgggt 124

<210> 49
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(147)
 <223> n = A,T,C or G

<400> 49
 gccgatgcta ctatttttatt gcaggagggtg ggggtgtttt tattattctc tcaacagctt 60
 tgtggctaca ggtggtgtct gactgcatna aaaantttt tacgggtgat tgcaaaaatt 120
 ttagggcacc catatcccaa gcantgt 147

<210> 50
 <211> 107
 <212> DNA
 <213> Homo sapien

<400> 50
 acattaaatt aataaaagga ctgttgggggt tctgctaaaa cacatggctt gatattattgc 60

atggtttgag gttaggagga gttaggcata tgttttgga gaggggt 107

<210> 51
 <211> 204
 <212> DNA
 <213> Homo sapien

<400> 51
 gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgacagg 60
 cgggaaggaa aggcagagaa gtgacaccgt cagggggaaa tgacagaaag gaaaatcaag 120
 gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttggcca 180
 cctccctttt gggaccagca atgt 204

<210> 52
 <211> 491
 <212> DNA
 <213> Homo sapien

<220> .
 <221> misc_feature
 <222> (1)...(491)
 <223> n = A,T,C or G

<400> 52
 acaaagataa catatatctt ataacaaaaa tttgatagtt ttaaagggtta gtattgtgta 60
 gggatatttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca 120
 ccatcagaca ggttttttaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa 180
 aaaacttctt gtatcaattt cttttgttca aaatgactga ctttaantatt tttaaatatt 240
 tcanaaacac ttctcaaaa attttcaana tggtagcttt canatgtnc ctcagtccca 300
 atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc 360
 atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat 420
 caattttatt tggataacaa aggggtctcca aatttatattg aaaaataaat ccaagttaat 480
 atcactcttg t 491

<210> 53
 <211> 484
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(484)
 <223> n = A,T,C or G

<400> 53
 acataattta gcagggtctaa ttaccataag atgctattta ttaanaggtn tatgatctga 60
 gtattaacag ttgctgaagt ttggtatttt tatgcagcat tttctttttg ctttgataac 120
 actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct 180
 caatcaaate tctacataac actatagtaa ttaaaacggt aaaaaaaagt gttgaaatct 240
 gactagtat anaccgtctc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc 300
 agcttttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct 360
 aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccnng 420
 tancttgant ctgtgtattc caggancagg cggtatggaat gggccagccc ncggatgttc 480
 cant 484

<210> 54
 <211> 151
 <212> DNA

<213> Homo sapien

<400> 54

```
actaaacctc gtgcttgtga actccatata gaaaacggtg ccatccctga acacggctgg      60
ccactgggta tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag      120
tctatgtcct ctcaagtgcc tttttgtttg t                                     151
```

<210> 55

<211> 91

<212> DNA

<213> Homo sapien

<400> 55

```
acctggcttg tctccgggtg gttcccggtg cccccacgg tccccagaac ggacactttc      60
gccctccagt ggatactcga gccaaagtgg t                                     91
```

<210> 56

<211> 133

<212> DNA

<213> Homo sapien

<400> 56

```
ggcgggatgtg cgttgggttat atacaaatat gtcattttat gtaagggact tgagtatact      60
tggatttttg gtatctgtgg gttgggggga cggtcagga accaatacc catggatacc      120
aagggacaac tgt                                     133
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<210> 57

<211> 147

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(147)

<223> n = A,T,C or G

<400> 57

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actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc      60
gactgggagc tgagcccttc cctttgcgcc tgccctcagag gattgttgcc gacntgcana      120
tctcantggg ctggatncat gcaggt                                     147
```

<210> 58

<211> 198

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(198)

<223> n = A,T,C or G

<400> 58

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acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc      60
tgattacata catttatcct ttaaaaaaga tgtaaatctt aatttttatg ccatctatta      120
atttaccaat gagttacctt gtaaatgaga agtcatgata gcaactgaatt ttaactagtt      180
ttgacttcta agtttggt                                     198
```

<210> 59

<211> 330
 <212> DNA
 <213> Homo sapien

<400> 59
 acaacaaatg ggttgtgagg aagtcttata agcaaaactg gtgatggcta ctgaaaagat 60
 ccattgaaaa ttatcattaa tgatttttaa tgacaagtta tcaaaaactc actcaatttt 120
 cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa 180
 tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagaccag 240
 cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt 300
 tttcgtcttt attggacttc tttgaagagt 330

<210> 60
 <211> 175
 <212> DNA
 <213> Homo sapien

<400> 60
 accgtgggtg ctttctacat tcctgacggc tccttcacca acatctgggt ctacttcggc 60
 gtogtgggtc ctttctctt catcctcatc cagctgggtc tgctcatcga ctttgccgac 120
 tcctggaacc agcgggtggc gggcaaggcc gaggagtgcg attcccgtgc ctggt 175

<210> 61
 <211> 154
 <212> DNA
 <213> Homo sapien

<400> 61
 accccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gagggtgagt 60
 ggttggttgc cttcaacagt atcctccctt ttccggatct gctgagccgg acagcagtcg 120
 tggactgcac agccccgggg ctccacattg ctgt 154

<210> 62
 <211> 30
 <212> DNA
 <213> Homo sapien

<400> 62
 cgctcgagcc ctatagttag tcgtattaga 30

<210> 63
 <211> 89
 <212> DNA
 <213> Homo sapien

<400> 63
 acaagtcatt tcagcaccct ttgtcttcca aaactgacca tcttttatat ttaatgcttc 60
 ctgtatgaat aaaaatgggt atgtcaagt 89

<210> 64
 <211> 97
 <212> DNA
 <213> Homo sapien

<400> 64
 accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag 60
 aatcagtga tccaggattg gtccttggat ctgggggt 97

<210> 65
 <211> 377
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(377)
 <223> n = A,T,C or G

<400> 65
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccctt tttgatggca 60
 gcatggcgct ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc 120
 ccaaccctgg tctaccacaca nttctggcta tgggctgtct ctgccactga acatcagggt 180
 tcggtcataa natgaaatcc caanggggac agaggtcagt agaggaagct caatgagaaa 240
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300
 tgggggtgaa ctacccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
 gggcgggagg agcatgt 377

<210> 66
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 66
 acgcctttcc ctccagaattc aggggaagaga ctgtgcgctg ccttcctccg ttgttgctg 60
 agaaccctgt tgcccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
 aggaactaac tgcacctgg tctctctccc agtccccagt tcacctcca tccctcacct 180
 tctccactc taagggatat caacactgac cagcacaggg gccctgaatt tatgtggttt 240
 ttatatattt ttttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300
 tgttt 305

<210> 67
 <211> 385
 <212> DNA
 <213> Homo sapien

<400> 67
 actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggc ctgagagttc 120
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
 tgtgctgtgc tggagattca cttttgagag agttctctcc tgagacctga tctttagagg 240
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300
 cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360
 catagtttct gtgctagtgg accgt 385

<210> 68
 <211> 73
 <212> DNA
 <213> Homo sapien

<400> 68
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
 gtttttttaa tgg 73

<210> 69
 <211> 536
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(536)

<223> n = A,T,C or G

<400> 69

actagtccag	tgtgggtggaa	ttccattgtg	ttgggggctc	tcaccctcct	ctcctgcagc	60
tccagctttg	tgctctgcct	ctgaggagac	catggcccag	catctgagta	ccctgctgct	120
cctgctggcc	accctagctg	tggccctggc	ctggagcccc	aaggaggagg	ataggataat	180
cccgggtggc	atctataacg	cagacctcaa	tgatgagtgg	gtacagcgtg	cccttcactt	240
cgccatcagc	gagtataaca	aggccaccaa	agatgactac	tacagacgtc	cgctgcgggt	300
actaagagcc	aggcaacaga	cogttggggg	ggtgaattac	ttcttcgacg	tagaggtggg	360
ccgaaccata	tgtaccaagt	cccagcccaa	cttggacacc	tgtgccttcc	atgaacagcc	420
agaactgcag	aagaaacagt	tgtgctcttt	cgagatctac	gaagttccct	ggggagaaca	480
gaangtcctt	gggtgaaatc	caggtgtcaa	gaaatcctan	ggatctgttg	ccaggc	536

<210> 70

<211> 477

<212> DNA

<213> Homo sapien

<400> 70

atgaccccta	acaggggccc	tctcagccct	cctaattgacc	tccggcctag	ccatgtgatt	60
tcacttccac	tccataacgc	tcctcatact	aggcctacta	accaacacac	taaccatata	120
ccaatgatgg	cgcgatgtaa	cacgagaaag	cacataccaa	ggccaccaca	caccacctgt	180
ccaaaaaggc	cttcgatacg	ggataatcct	atattattacc	tcagaagttt	ttttcttcgc	240
agggattttt	ctgagccctt	taccactcea	gcctagcccc	taccccccaa	ctaggagggc	300
actggccccc	aacaggcatc	accccgcata	atcccctaga	agtcccactc	ctaaacacat	360
ccgtattact	cgcatcagga	gtatcaatca	cctgagctca	ccatagtcta	atagaaaaca	420
accgaaacca	aattattcaa	agcactgctt	attacaattt	tactgggtct	ctatttt	477

<210> 71

<211> 533

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(533)

<223> n = A,T,C or G

<400> 71

agagctatag	gtacagtgtg	atctcagctt	tgcaaacaca	ttttctacat	agatagtact	60
aggtattaat	agatatgtaa	agaaagaaat	cacaccatta	ataatggtaa	gattgggtta	120
tgtgatttta	gtggattttt	tggcaccctt	atatatgttt	tccaaacttt	cagcagtgat	180
attattttcca	taacttaaaa	agtgagtttg	aaaaagaaaa	tctccagcaa	gcattctcatt	240
taaataaagg	tttgtcatct	ttaaaaatac	agcaatatgt	gactttttta	aaaagctgtc	300
aaatagggtg	gaccctacta	ataattatta	gaaatacatt	taaaaacatc	gagtacctca	360
agtcagtttg	ccttgaaaaa	tatcaaatat	aactcttaga	gaaatgtaca	taaaagaatg	420
cttcgtaatt	ttggagtang	aggttccctc	ctcaattttg	tattttttaa	aagtacatgg	480
taaaaaaaaa	aattcacac	agtatataag	gctgtaaaaa	gaagaattct	gcc	533

<210> 72

<211> 511

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(511)
 <223> n = A,T,C or G

<400> 72
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcggtga 60
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120
 aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga 180
 aaacatggan agattgggtgc tgganatcgc cgtggctatt cctcattgtt attacanagt 240
 gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420
 atttctctcc attgcagcna naaacccgtt cttctaagca aacncagggtg atgatggcna 480
 aaatacaccc cctcttgaag naccnggagg a 511

<210> 73
 <211> 499
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(499)
 <223> n = A,T,C or G

<400> 73
 cagtgcagc actggtgccca gtaccagtag caataacagt gccagtgccca gtgccagcac 60
 cagtgggtggc ttccagtgtg gtgccagcct gaccgccact ctcacatttg ggctcttcgc 120
 tggccttggg ggagctgggt ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180
 caagtggatg tttagatatt gttaatcctg ccagtctttc tcttcaagcc aggggtgcac 240
 ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300
 ctctgcatga aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggc cggccgctcg 360
 antctagagg gcccggttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420
 catctgttgt ttgcccctcc cccgntgcct tccttgaccc tggaaagtgc cactcccat 480
 gtcctttcct aantaaaat 499

<210> 74
 <211> 537
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(537)
 <223> n = A,T,C or G

<400> 74
 tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gogaagagat 60
 ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact 120
 tccaggccca oggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180
 cattgtatgc atggaaacat ggaggaacag tattacagtg toctaccact ctaatcaaga 240
 aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300
 ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc 360
 cagtttgctt gatataattg ttgatattaa gattcttgac ttatattttg aatgggttct 420
 actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480
 tctacaatgt agaaaatgaa ggaaatgcc caaattgtat ggtgataaaa gtcccggt 537

28

<210> 75
 <211> 467
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(467)
 <223> n = A,T,C or G

<400> 75
 caaanacaat tgttcaaaag atgcaaatag tacactactg ctgcagctca caaacacctc 60
 tgcataattac acgtacctcc tcctgctcct caagtagtgt ggtctatattt gccatcatca 120
 cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
 tggcacaagg aggccatctt ttctcatcgc gttattgtcc ctagaagcgt cttctgagga 240
 tctagtggg ctttctttct gggtttgggc catttcantt ctcagtgtgtg tactattcta 300
 tcattattgt ataacggttt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
 caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420
 ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76
 <211> 400
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(400)
 <223> n = A,T,C or G

<400> 76
 aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgcctac 60
 tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120
 atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg ttatcatccat 180
 ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagt gagcattcag 240
 acttgtcttt cagcaaggac tgggtctttct atctcttgta ctacactgaa ttcaccccca 300
 ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
 ttnagtggga tcganacatg taagcagcan catgggaggt 400

<210> 77
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 77
 ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
 ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgtctc 120
 caggcactgt tcattctcagc ttttctgtcc ctttgtctcc ggcaagcgt tctgtctgaa 180
 gttcatatct ggagcctgat gtcttaacga ataaaggtcc catgctccac ccgaaaaaaa 240
 aaaaaaaa 248

<210> 78
 <211> 201
 <212> DNA
 <213> Homo sapien

<400> 78

actagtccag	tgtgggtggaa	ttccattgtg	ttgggcccac	cacaatggct	acotttaaca	60
tcacccagac	cccgcctgc	cogtgcccca	cgctgctgct	aacgacagta	tgatgcttac	120
tctgctactc	ggaaactatt	tttatgtaat	taatgtatgc	tttcttggtt	ataaatgcct	180
gatttaaaaa	aaaaaaaaa	a				201

<210> 79
 <211> 552
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(552)
 <223> n = A,T,C or G

<400> 79						
tccttttgtt	agggttttga	gacaacccta	gacctaaact	gtgtcacaga	cttctgaatg	60
tttaggcagt	gctagtaatt	tcctcgtaat	gattctgtta	ttacttttct	attctttatt	120
cctctttctt	ctgaagatta	atgaagttga	aaattgaggt	ggataaatac	aaaaaggtag	180
tgtgatagta	taagtatcta	agtgcagatg	aaagtgtgtt	atatatatcc	attcaaaatt	240
atgcaagtta	gtaattactc	agggttaact	aaattacttt	aatatgctgt	tgaacctact	300
ctgttccttg	gctagaaaaa	attataaaca	ggactttgtt	agtttgggaa	gccaaattga	360
taatattcta	tgttctaaaa	gttgggctat	acataaanta	tnaagaaata	tggaatttta	420
ttcccaggaa	tatgggggtc	atztatgaat	antacccggg	anagaagttt	tgantnaaac	480
cngttttggt	taatacgtta	atatgtcctn	aatnaacaag	gcntgactta	tttccaaaaa	540
aaaaaaaaaa	aa					552

<210> 80
 <211> 476
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 80						
acagggattt	gagatgctaa	ggccccagag	atcgtttgat	ccaaccctct	tattttcaga	60
ggggaaaaatg	gggcctagaa	gttacagagc	atctagctgg	tgcgctggca	cccctggcct	120
cacacagact	cccagtagc	tgggactaca	ggcacacagt	cactgaagca	ggccctgttt	180
gcaattcacg	ttgccacctc	caacttaaac	attcttcata	tgtgatgtcc	ttagtcacta	240
aggttaaaact	ttccccacca	gaaaaggcaa	cttagataaa	atcttagagt	actttcatac	300
tcttctaagt	cctcttccag	cctcactttg	agtcctcctt	gggggttgat	aggaantntc	360
tcttggtttt	ctcaataaaa	tctctatcca	tctcatgttt	aatttggtac	gcntaaaaat	420
gctgaaaaaa	ttaaaatggt	ctggtttcnc	tttaaaaaaa	aaaaaaaaaa	aaaaaa	476

<210> 81
 <211> 232
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(232)
 <223> n = A,T,C or G

<400> 81

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tttttttttg tatgcntcn ctgtgnggtt attgttgctg ccaccctgga ggagcccagt    60
ttcttctgta tctttctttt ctgggggatc ttcttggtc tgccctcca ttcccagcct    120
ctcatcccca tcttgcaact ttgctagggg ttggaggcgt ttcttggtag cccctcagag    180
actcagtcag cgggaataag tcctaggggt ggggggtgtg gcaagccggc ct          232

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<210> 82
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

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```

<400> 82
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc    60
agtaccagta ccaataacat gccagtgccg gtgccagcac cagtgggtggc ttcagtgtctg    120
gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggt ggagctgggtg    180
ccagcaaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt    240
gttaatcctg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac    300
agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg    360
ccatttcaaa aaaaaaaaaa aaa          383

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<210> 83
<211> 494
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(494)
<223> n = A,T,C or G

```

```

<400> 83
accgaattgg gaccgtggc ttataagcga tcatgtcctc cagtattacc tcaacgagca    60
gggagatcga gtctatacgc tgaagaaatt tgaccgatg ggacaacaga cctgtctcagc    120
ccatcctgct cgttctctcc cagatgacaa atactctcga caccgaatca ccatcaagaa    180
acgcttcaag gtgtcatga cccagcaacc gcgccctgtc ctctgagggg ccttaacttg    240
atgtcttttc tgccacctgt taccctcggg agactccgta accaaactct tcggactgtg    300
agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat    360
tatgcttggt tgaggcaatc atggtggcat caccatnaa gggaacacat ttganttttt    420
tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta    480
aaaaaaaaaa aaaa          494

```

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<210> 84
<211> 380
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

```

```

<400> 84
gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca    60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag    120

```

gaggacatgg	acgtggccct	catggagcac	agcaactgct	cgtcggagcc	cggcttctgg	180
gcacaccctc	ctggggccca	ggcgggcacc	tgcgtctccc	agtatgcaa	ctggctgggtg	240
gtgctgctcc	tcgtcatctt	cctgctcgtg	gccaacatcc	tgctggtcac	ttgctcattg	300
ccatgttcag	ttacacattc	ggcaaagtac	agggcaacag	cnatctctac	tggaaggcc	360
agcgttnccg	cctcatccgg					380

<210> 85
 <211> 481
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(481)
 <223> n = A,T,C or G

<400> 85						
gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cctcctgcat	cttggggcgg	ctaatatcca	120
ggaaactctc	aatcaagtca	ccgtcnatna	aacctgtggc	tggttctgtc	ttccgctcgg	180
tgtgaaagga	tctccagaag	gagtgtctga	tcttccccac	acttttgatg	actttattga	240
gtcgattctg	catgtccagc	aggaggttgt	accagctctc	tgacagtga	gtcaccagcc	300
ctatcatgcc	nttgaacgtg	ccgaagaaca	ccgagccttg	tgtggggggg	gnagtctcac	360
ccagattctg	cattaccaga	nagccgtggc	aaaaganatt	gacaactcgc	ccaggngaa	420
aaagaacacc	tcctggaagt	gctngccgct	cctcgtccnt	tggtggnggc	gcntnccttt	480
t						481

<210> 86
 <211> 472
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(472)
 <223> n = A,T,C or G

<400> 86						
aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgctg	agaattcatt	60
acttggaaaa	gcaacttnaa	gcctggacac	tggtattaaa	attcacaata	tgcaacactt	120
taaacagtgt	gtcaatctgc	tcccttactt	gtcatcacc	agtctgggaa	taagggtatg	180
ccctattcac	acctgttaaa	agggcgctaa	gcatttttga	ttcaacatct	ttttttttga	240
cacaagtcog	aaaaaagcaa	aagtaaacag	ttnttaattt	gttagccaat	tcactttctt	300
catgggacag	agccatttga	tttaaaaagc	aaattgcata	atattgagct	ttgggagctg	360
atatntgagc	ggaagantag	cctttctact	tcaccagaca	caactccttt	catattggga	420
tgtnnacnaa	agttatgtct	cttacagatg	ggatgctttt	gtggcaattc	tg	472

<210> 87
 <211> 413
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(413)
 <223> n = A,T,C or G

<400> 87

```

agaaccaggt atctctnaaa acaacctctc ataccttggt gacctaatTT tgtgtgcgtg      60
tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg      120
cctcttttgg atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct      180
ttgtcttctg tgtaaagtgt actagagaaa acacctatnt tatgagtcaa tctagttingt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg      300
ggggacaaaag aaaagcnaaa ctgaacatna gaaacaattn cctggtgaga aattncataa      360
acagaaattg ggtngtatat tgaaanannng catcattnaa acgttttttt ttt              413

```

```

<210> 88
<211> 448
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(448)
<223> n = A,T,C or G

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<400> 88
cgcagcgggt cctctctatc tagctccagc ctctgcctg ccccaactccc cgcgtcccgc      60
gtcctagccn accatggccg ggcccctgcg cgcccgcgtg ctctgtctgg ccacccctggc      120
cgtggccctg gccgtgagcc ccgcggccgg ctccagctcc ggcaagccgc cgcgcctggt      180
gggaggccca tggaccccg cgtggaagaag aaggtgtgcg gcgtgcactg gactttgccg      240
tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgtctgag gttgtgccgc      300
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng      360
tttaccagaa ccnagccaat tngaacaatt nccccctcat aacagcccct tttaaaaagg      420
gaancantcc tgntcttttc caaatTTT              448

```

```

<210> 89
<211> 463
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(463)
<223> n = A,T,C or G

```

```

<400> 89
gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca      60
gtagtgaattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc      120
agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt      180
ctcagtgaca agttntttct gatgcgaagt tctnattcca gtgttttagt cttttgcac      240
tttnatgtnn agacttgccct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg      300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn      360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn      420
aattcnana anttcagntn tcatacaaca naacngganc ccc              463

```

```

<210> 90
<211> 400
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(400)
<223> n = A,T,C or G

```

```

<400> 90
agggattgaa ggtctntnt actgtcggac tgttcancca ccaactctac aagttgctgt      60
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaaat      120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttcact      180
tcctttgtta agacttcate tggtaaagtc ttaagttttg tagaaaggaa ttttaattgct      240
cgttctctaa caatgtcctc tccttgaagt atttggtgta acaaccacc tnaagtcctt      300
ttgtgcatcc attttaata tacttaatag ggcattggtt cactagggtt aattctgcaa      360
gagtcactgt tctgcaaaag ttgcgttagt atatctgccca      400

```

```

<210> 91
<211> 480
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(480)
<223> n = A,T,C or G

```

```

<400> 91
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact      60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac      120
atgcctcttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nccgctctt      180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttaciaat tcacccacga      240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt      300
tgtcaatact aaccgctgg tttgcctcca tcacatttgt gatctgtagc tctggatata      360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt      420
ngatcaggtt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa      480

```

```

<210> 92
<211> 477
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(477)
<223> n = A,T,C or G

```

```

<400> 92
atacagccca natcccacca cgaagatgag cttgttgact gagaacctga tgcgggtcact      60
ggtccccgtg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt      120
cccacgcagg cagcagcggg gccgggtcaat gaactccact cgtgggttgg ggttgacggg      180
taantgcagg aagaggctga ccacctcgcg gtccaccagg atgcccagc gtgcgggacc      240
tgcagcgaaa ctctctgatg gtcattgagc ggaagcgaat gangcccagg gccttgccca      300
gaaccttccg cctgttctct ggcgtcacct gcagctgctg ccgctnacac tcggcctcgg      360
accagcggac aaacggcggt gaacagccgc acctcacgga tgcccantgt gtcgcgctcc      420
aggaacggcn ccagcgtgtc cagggtcaatg tcggtgaanc ctccgcgggt aatggcg      477

```

```

<210> 93
<211> 377
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = A,T,C or G

```

```

<400> 93
gaacggctgg accttgccctc gcattgtgct gctggcagga ataccttggc aagcagctcc      60
agtccgagca gccccagacc gctgccgccc gaagctaagc ctgcctctgg ccttcccctc      120
cgctcaatg cagaaccant agtgggagca ctgtgttttag agttaagagt gaacactgtn      180
tgattttact tgggaatttc ctctgttata tagcttttcc caatgctaata ttccaaacaa      240
caacaacaaa ataacatggt tgcctgttna gttgtataaaa agtangtgat tctgtatnta      300
aagaaaatat tactgttaca tatactgctt gcaantttctg tattttattgg tnctctggaa      360
ataaatatat tattaa                                     377

```

```

<210> 94
<211> 495
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(495)
<223> n = A,T,C or G

```

```

<400> 94
ccctttgagg ggtagggctc cagttcccag tggagaagaa aggccaggag aantgcgtgc      60
cgagctgang cagatttccc acagtgaccc cagagccctg ggctatagtc tctgaccctc      120
ccaaggaaag accaccttct ggggacatgg gctggagggc aggacctaga ggcaccaagg      180
gaaggcccca ttccggggct gttccccgag gaggaaggga aggggctctg tgtgcccccc      240
acgaggaana ggccctgant cctgggatca nacaccctt cactgtatc cccacacaaa      300
tgcaagctca ccaaggtccc ctctcagtc cttccctaca ccctgaacgg nactggccc      360
acaccacccc agancancca cccgccatgg ggaatgttct caaggaatcg cngggcaacg      420
tggactctng tccnnaagg gggcagaatc tccaatagan gganngaacc cttgctnana      480
aaaaaaaaana aaaaa                                     495

```

```

<210> 95
<211> 472
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

```

```

<400> 95
ggttacttgg ttctattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt      120
tagctgtttt gagttgattc gcaccactgc accacaactc aatatgaaaa ctatttnact      180
tattttattat cttgtgaaaa gtatacaatg aaaattttgt tcatactgta tttatcaagt      240
atgatgaaaa gcaatagata tatattcttt tattatgttn aattatgatt gccattatta      300
atcggaacaaa tgtggagtgt atgttctttt cacagtaata tatgcctttt gtaacttcac      360
ttggttattt tattgtaaat gaattacaaa attcttaatt taagaaaatg gtangttata      420
tttanttcan taatttcttt ccttgtttac gttaattttg aaaagaatgc at              472

```

```

<210> 96
<211> 476
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```

35

<222> (1)...(476)

<223> n = A,T,C or G

<400> 96

ctgaagcatt	tcttcaaact	tntctacttt	tgtcattgat	acctgtagta	agttgacaat	60
gtggtgaaat	ttcaaaaatta	tatgtaactt	ctactagttt	tactttctcc	cccaagtctt	120
ttttaactca	tgattttttac	acacacaatc	cagaacttat	tatatagcct	ctaagtcttt	180
attcttcaca	gtagatgatg	aaagagtcct	ccagtgtctt	gngcanaatg	ttctagntat	240
agctggatac	atacngtggg	agttctataa	actcatacct	cagtgggact	naacccaaaat	300
tgtgttagtc	tcaattccta	ccacactgag	ggagcctccc	aaatcactat	attcttatct	360
gcaggctactc	ctccagaaaa	acngacaggg	caggcttgca	tgaaaaagtn	acatctgcgt	420
tacaaagtct	atcttcctca	nangtctgtt	aaggaacaat	ttaatcttct	agcttt	476

<210> 97

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(479)

<223> n = A,T,C or G

<400> 97

actctttcta	atgctgatat	gatcttgagt	ataagaatgc	atatgtcact	agaatggata	60
aaataatgct	gcaaaacttaa	tggtcttatg	caaaatggaa	cgctaatagaa	acacagctta	120
caatcgcaaa	tcaaaactca	caagtgtctca	tctgtttag	atttagtgta	ataagactta	180
gattgtgctc	cttcggatat	gattgtttct	canatcttgg	gcaatnttcc	ttagtcaa	240
caggctacta	gaattctggt	attggatatn	tgagagcatg	aaatttttaa	naatacactt	300
gtgattatna	aattaatcac	aaatttcact	tatacctgct	atcagcagct	agaaaaacat	360
ntnmttttta	natcaagta	ttttgtgttt	ggaantgttn	aaatgaaatc	tgaatgtggg	420
ttcnatctta	ttttttcccn	gacnactant	tnctttttta	gggnctattc	tgancctac	479

<210> 98

<211> 461

<212> DNA

<213> Homo sapien

<400> 98

agtgacttgt	cctccaacaa	aacccttga	tcaagtttgt	ggcactgaca	atcagaccta	60
tgctagtctc	tgctacttat	tcgctactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaactctatt	cctacttgta	cggactttga	180
agtgattcag	tttcctctac	ggatgagaga	ctggctcaag	aatatcctca	tgcagcttta	240
tgaagccact	ctgaacacgc	tggttatcta	gatgagaaca	gagaaataaa	gtcagaaaaat	300
ttacctggag	aaaagaggct	ttggctgggg	accatcccat	tgaaccttct	cttaaggact	360
ttaagaaaaa	ctaccacatg	ttgtgtatcc	tggtgccggc	cgtttatgaa	ctgaccaccc	420
tttggaataa	tcttgacgct	cctgaacttg	ctcctctgcg	a		461

<210> 99

<211> 171

<212> DNA

<213> Homo sapien

<400> 99

gtggccgcgc	gcaggtgttt	cctcgtaccg	cagggccccc	tcccttcccc	aggcgtccct	60
ggcgccctct	gcgggcccga	ggaggagcgg	ctggcggtg	gggggagtgt	gaccacccct	120
cggtgagaaa	agccttctct	agcgatctga	gaggcgtgcc	ttgggggtac	c	171

36

<210> 100
 <211> 269
 <212> DNA
 <213> Homo sapien

<400> 100
 cgcccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc 60
 cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc 120
 aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga 180
 cagccggaac agagcccggg gaagcgggag gcctcgggga gccctcggg aagggcggcc 240
 cgagagatac gcaggtgcag gtggccgcc 269

<210> 101
 <211> 405
 <212> DNA
 <213> Homo sapien

<400> 101
 tttttttttt ttttggaaac tactgcgagc acagcaggtc agcaacaagt ttattttgca 60
 gctagcaagg taacagggtg gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg 120
 ttgattgggt tgtctttatg ggggcggggg ggggtagggg aaacgaagca aataacatgg 180
 agtgggtgca cctccctgt agaacctggt tacaagcct ggggcagttc acctggtctg 240
 tgaccgtcat tttcttgaca tcaatgttat tagaagtcag gatattcttt agagagtcca 300
 ctgttctgga gggagattag ggtttcttgc caaatccaac aaaatccact gaaaaagtgt 360
 gatgatcagt acgaataccg aggcattatc tcatatcggt ggcca 405

<210> 102
 <211> 470
 <212> DNA
 <213> Homo sapien

<400> 102
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
 ggcacttaat ccatttttat ttcaaaatgt ctacaaattt aatcccatta tacggtattt 120
 tcaaaatcta aattattcaa attagccaaa tccttaccaa ataataccca aaaatcaaaa 180
 atatacttct ttcagcaaac ttgttacata aattaaaaaa atatatacgg ctgggtgtttt 240
 caaagtacaa ttatcttaac actgcaaaca ttttaaggaa ctaaaataaa aaaaaacact 300
 ccgcaaaggg taaagggaac aacaaattct tttacaacac cattataaaa atcatatctc 360
 aaatcttagg ggaatatata cttcacacgg gatcttaact ttactcact ttgtttattt 420
 ttttaaacca ttgtttgggc ccaacacaat ggaatcccc ctggactagt 470

<210> 103
 <211> 581
 <212> DNA
 <213> Homo sapien

<400> 103
 tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttatttttact 60
 tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac 120
 taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt 180
 gaaaatcttc cttagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc 240
 atttttcttg tctttaaaat tatctaactt ttccattttt tccctattcc aagtcatttt 300
 gcttctctag cctcatttcc tagctcttat ctactattag taagtggcct ttttcctaaa 360
 agggaaaaca ggaagagaaa tggcacacaa aacaaacatt ttatattcat atttctacct 420
 acgttaataa aatagcattt tgtgaagcca gctcaaaaga aggcttagat ccttttatgt 480
 ccatttttagt cactaaacga tatcaaagtg ccagaatgca aaaggtttgt gaacatttat 540
 tcaaaagcta atataagata tttcacatac tcatctttct g 581

37

<210> 104
 <211> 578
 <212> DNA
 <213> Homo sapien

<400> 104
 tttttttttt tttttttttt tttttctctt cttttttttt gaaatgagga tgcagttttt 60
 cactctctag atagggcatg aagaaaactc atctttccag ctttaaaata acaatcaaat 120
 ctcttatgct atatcatatt ttaagttaaa ctaatgagtc actggcttat cttctcctga 180
 aggaaatctg ttcattcttc tcattcatat agttatatca agtactacct tgcattatga 240
 gaggtttttt ttctctatatt acacatatat ttccatgtga atttgtatca aacctttatt 300
 ttcatgcaaa ctagaaaata atgtttcttt tgcataagag aagagaacaa tatagcatta 360
 caaaactgct caaattgttt gttaagttaa ccattataat tagttggcag gagctaatac 420
 aaatcacatt tacgacagca ataataaaac tgaagtacca gttaaatatc caaaataatt 480
 aaaggaacat ttttagcctg ggtataatta gctaattcac tttacaagca tttattagaa 540
 tgaattcaca tgttattatt cctagcccaa cacaatgg 578

<210> 105
 <211> 538
 <212> DNA
 <213> Homo sapien

<400> 105
 tttttttttt tttttcagta ataatcagaa caatatttat ttttatattt aaaattcata 60
 gaaaagtgc ttacatttaa taaaagtttg tttctcaaag tgatcagagg aattagatat 120
 gtcttgaaca ccaatattaa tttgaggaaa atacacaaa atacattaag taaattattt 180
 aagatcatag agcttgtaag tgaaaagata aaatttgacc tcagaaactc tgagcattaa 240
 aaatccacta ttagcaaaata aattactatg gacttcttgc ttttaattttg tgatgaatat 300
 ggggtgtcac tggtaaaccac acacattctg aaggatacat tacttagtga tagattctta 360
 tgtactttgc taatacgtgg atatgagttg acaagtttct ctttcttcaa tcttttaagg 420
 ggcgagaaat gaggaagaaa agaaaaggat tacgcatact gttctttcta tggaaggatt 480
 agatatgttt cctttgccaa tattaaaaaa ataataatgt ttactactag tgaaaccc 538

<210> 106
 <211> 473
 <212> DNA
 <213> Homo sapien

<400> 106
 tttttttttt ttttttagtc aagtttctat ttttattata attaaagtct tggtcatttc 60
 atttattagc tctgcaactt acatatttaa attaaagaaa cgtttttagac aactgtacaa 120
 tttataaatg taagggtgcca ttattgagta atatattcct ccaagagtgg atgtgtccct 180
 tctcccacca actaatgaac agcaacatta gtttaatttt attagtagat atacactgct 240
 gcaaacgcta attctcttct ccatcccat gtgatatgtg gtatatgtgt gagttggtag 300
 aatgcatcac aatctacaat caacagcaag atgaagctag gctgggcttt cggtgaaaat 360
 agactgtgtc tgtctgaatc aaatgatctg acctatcctc ggtggcaaga actcttcgaa 420
 ccgcttcctc aaaggcgctg ccacatttgt ggctctttgc acttgtttca aaa 473

<210> 107
 <211> 1621
 <212> DNA
 <213> Homo sapien

<400> 107
 cgccatggca ctgcagggca tctcggtcac ggagctgtcc ggccctggccc cgggcccggtt 60
 ctgtgctatg gtcctggctg acttcggggc gcgtgtggta cgcggtggacc ggcccggtc 120
 ccgctacgac gtgagccgct tgggcccggg caagcgctcg ctagtgtctg acctgaagca 180
 gccgcgggga gccgcgctgc tgcggcgtct gtgcaagcgg tcggatgtgc tgctggagcc 240

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cttccgccgc ggtgtcatgg agaaactcca gctgggcccc gagattctgc agcgggaaaa 300
tccaaggctt atttatgcca ggctgagtggt atttggccag tcaggaagct tctgccggtt 360
agctggccac gatatcaact atttggcttt gtcagggtgtt ctctcaaaaa ttggcagaag 420
tggtgagaat ccgtatgccc cgctgaatct cctggctgac tttgctggtg gtggccttat 480
gtgtgcactg ggcattataa tggctctttt tgaccgcaca cgactgaca agggtcaggt 540
cattgatgca aatatggtgg aaggaacagc atatttaagt tcttttctgt ggaaaactca 600
gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt 660
ctatacgact tacaggacag cagatgggga attcatggct gttggagcaa tagaacccca 720
gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaacttc ccaatcagat 780
gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac 840
gaaggcagag tgggtgcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac 900
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cagccgcgaa gagattttatc agcttaactc agataaaatc attgaaagta ataaggtaaa 1140
agctagtctc taacttccag gccacgggt caagtgaatt tgaatactgc atttacagt 1200
tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta 1260
ccactcta atcaagaaaaga attacagact ctgattctac agtgatgatt gaattctaaa 1320
aatggttattc attagggctt ttgatttata aaactttggg tacttatact aaattatggt 1380
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ttttgaatgg gttctagtga aaaaggaatg atatatctt gaagacatcg atatacattt 1500
atttacactc ttgattctac aatgtagaaa ataggaaaat gccacaaaatt gtatggtgat 1560
aaaagtcacg tgaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
a

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<210> 108
<211> 382
<212> PRT
<213> Homo sapien

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```

<400> 108
Met Ala Leu Gln Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1 5 10 15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20 25 30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35 40 45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50 55 60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65 70 75 80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85 90 95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100 105 110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115 120 125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130 135 140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145 150 155 160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165 170 175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180 185 190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195 200 205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg

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210	215	220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala	Ile Glu Pro Gln Phe	
225	230	235
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys	Ser Asp Glu Leu Pro	240
	245	250
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met	Lys Lys Lys Phe Ala	255
	260	265
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp	Cys Gln Ile Phe Asp	270
	275	280
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr	Phe Glu Glu Val Val	285
	290	295
His His Asp His Asn Lys Glu Arg Gly Ser Phe	Ile Thr Ser Glu Glu	300
305	310	315
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu	Leu Asn Thr Pro Ala	320
	325	330
Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly	Glu His Thr Glu Glu	335
	340	345
Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu	Ile Tyr Gln Leu Asn	350
	355	360
Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys	Ala Ser Leu	365
370	375	380

<210> 109
 <211> 1524
 <212> DNA
 <213> Homo sapien

<400> 109
 ggcacgaggg tgcgccaggg cctgagcgga ggcgggggca gcctcgccag cggggggccc 60
 gggcctggcc atgcctcaact gagccagcgc ctgcgcctct acctcgccga cagctggaac 120
 cagtgcgacc tagtggtctt cacctgtctt ctctctggcg tgggctgccg gctgaccccg 180
 gggttggtacc acctgggccc cactgtcttc tgcctgcagt tcatggtttt caagggtgcg 240
 ctgcttcaca tcttcacggt caacaaacag ctggggccca agatcgtcct cgtgagcaag 300
 atgatgaagg acgtgttctt ctctctcttc ttctctggcg tgtggctggt agcctatggc 360
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 gtcttctacc gtccctacct gcagatcttc gggcagattc cccaggagga catggacgtg 480
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<210> 110
 <211> 3410
 <212> DNA

<213> Homo sapien

<400> 110

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaataa aaaaaaaaaa 3410

<210> 111
 <211> 1289
 <212> DNA
 <213> Homo sapien

<400> 111
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 tcatgcagc cggcgttggt gtctttgtct ttgggttctt gggctgctat ggtgctaaga 360
 ctgagagcaa gtgtgccctc gtgacgttct tcttcacact cctcctcatc ttcattgctg 420
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 ggaacaccac catgaaaggg ctcaagtgtc gtggcttcac caactatacg gattttgagg 600
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 ccaacacagc caatgaaacc tgcaccaagc aaaaggctca cgaccaaaaa gtagagggtt 720
 gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag 780
 ctggaattgg gggcctcgag ctggctgccca tgattgtgtc catgtatctg tactgcaatc 840
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 aagtgaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc 1260
 tgttacaatg ttaaaaaaaa aaaaaaaaaa 1289

<210> 112
 <211> 315
 <212> PRT
 <213> Homo sapien

<400> 112
 Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1 5 10 15
 Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
 20 25 30
 Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
 35 40 45
 Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
 50 55 60
 Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
 65 70 75 80
 Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
 85 90 95
 Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
 100 105 110
 Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
 115 120 125
 Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
 130 135 140
 Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
 145 150 155 160

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Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
 165 170 175
 Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
 180 185 190
 Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
 195 200 205
 His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
 210 215 220
 Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
 225 230 235 240
 Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
 245 250 255
 Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
 260 265 270
 Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
 275 280 285
 Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300
 Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

<210> 113
 <211> 553
 <212> PRT
 <213> Homo sapien

<400> 113
 Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
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 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30
 Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
 35 40 45
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80
 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110
 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu

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                245                250                255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
                260                265                270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
                275                280                285
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
                290                295                300
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
305                310                315                320
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
                325                330                335
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
                340                345                350
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
                355                360                365
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
                370                375                380
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
385                390                395                400
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
                405                410                415
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
                420                425                430
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
                435                440                445
Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
                450                455                460
Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
465                470                475                480
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
                485                490                495
Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
                500                505                510
Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
                515                520                525
Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
530                535                540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545                550

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<210> 114
<211> 241
<212> PRT
<213> Homo sapien

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<400> 114
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
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Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
20      25
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
35      40      45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
50      55      60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65      70      75      80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
85      90      95

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Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
 100 105 110
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
 115 120 125
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
 130 135 140
 Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
 145 150 155 160
 Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
 165 170 175
 Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
 180 185 190
 His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
 195 200 205
 Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
 210 215 220
 Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
 225 230 235 240
 Gln

<210> 115
 <211> 366
 <212> DNA
 <213> Homo sapien

<400> 115
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 ttggtttgtg aatccatctt gctttttccc catttggaact agtcattaac ccatctctga 180
 actggttagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggg 240
 tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300
 tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt 360
 ttagtc 366

<210> 116
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G

<400> 116
 acaaagatga accatttcct atattatagc aaaattaaaa tctaccogta ttctaattatt 60
 gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa 120
 agactttact attttcatat tttaagacac atgatttatc ctatttttagt aacctgggtc 180
 atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt 240
 tcaatctnga actatctana tcacagacat ttctatttcct tt 282

<210> 117
 <211> 305
 <212> DNA
 <213> Homo sapien

<220>

45

<221> misc_feature
 <222> (1)...(305)
 <223> n = A,T,C or G

<400> 117
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 tattttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120
 aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga 180
 tactgatccc tgatcactgt cctaatagcag gatgtgggaa acagatgagg tcacctctgt 240
 gactgccccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300
 tgggt 305

<210> 118
 <211> 71
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(71)
 <223> n = A,T,C or G

<400> 118
 accaagggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa 60
 aantcctggg t 71

<210> 119
 <211> 212
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(212)
 <223> n = A,T,C or G

<400> 119
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 gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120
 agtaagctgg ccctttctaataaaaagaaaat tgaaagggtt ctcactaanc ggaattaant 180
 aatggantca aganactccc aggcctcagc gt 212

<210> 120
 <211> 90
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(90)
 <223> n = A,T,C or G

<400> 120
 actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tgggtcttgcc 60
 ctccgccggc gcagaacatg ctggggtgggt 90

<210> 121
 <211> 218

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(218)
<223> n = A,T,C or G

<400> 121
tgtancgtga anacgacaga nagggttgtc aaaaatggag aanccttgaa gtcattttga 60
gaataagatt tgctaaaaga tttgggggcta aaacatgggtt attgggagac atttctgaag 120
atatncangt aaattangga atgaattcat gggtctttttt ggaattcctt tacgatngcc 180
agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122
<211> 171
<212> DNA
<213> Homo sapien

<400> 122
taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60
catttgtag ctcatggaac aggaagtcgg atggtggggc atcttcagtg ctgcatgagt 120
caccaccccg gcgggggtcat ctgtgccaca ggtccctgtt gacagtgcgg t 171

<210> 123
<211> 76
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(76)
<223> n = A,T,C or G

<400> 123
tgtagcgtga agachacaga atggtgtgtg ctgtgctatc caggaacaca tttattatca 60
ttatcaanta ttgtgt 76

<210> 124
<211> 131
<212> DNA
<213> Homo sapien

<400> 124
acctttcccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt 60
caatgtgtcg ggcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120
ttaagatttg t 131

<210> 125
<211> 432
<212> DNA
<213> Homo sapien

<400> 125
actttatcta ctggctatga aatagatggt ggaaaattgc gttaccaact ataccactgg 60
cttgaaaaag aggtgatagc tcttcagagg acttgtgact tttgtcaga tgctgaagaa 120
ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat 180
ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240

47

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ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc 300
catggtgggg gtcttgcacg tgtaagaatg gaattgattt tgcttttgca agaattctcag 360
caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccctc agtgcctctc 420
ctctttgctt gt 432

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<210> 126
<211> 112
<212> DNA
<213> Homo sapien

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<400> 126
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60
agtaagaatg atatttcccc ccagggatca ccaaataattt ataaaaattt gt 112

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<210> 127
<211> 54
<212> DNA
<213> Homo sapien

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<400> 127
accacgaaac cacaacaag atggaagcat caatccactt gccaaacaca gcag 54

```

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<210> 128
<211> 323
<212> DNA
<213> Homo sapien

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<400> 128
acctcattag taattgtttt gttgtttcat ttttttctaa tgtctccoct ctaccagctc 60
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgtcga 120
ttctctctga agtctaggtt acccattttg gggaccattt ataggcaata aacacagttc 180
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt 240
ttcctgcaaa aggtcactc agtcccttgc ttgtcagtg gactgggctc cccagggcct 300
aggctgcctt cttttccatg tcc 323

```

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<210> 129
<211> 192
<212> DNA
<213> Homo sapien

```

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<220>
<221> misc_feature
<222> (1)...(192)
<223> n = A,T,C or G

```

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<400> 129
acatacatgt gtgtatatat ttaaatatca cttttgtatc actctgactt tttagcatac 60
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120
tagcacattc atctgtgata naaagatagg tgagtttcat ttctttcacg ttggccaatg 180
gataaacaat gt 192

```

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<210> 130
<211> 362
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

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<222> (1)...(362)

<223> n = A,T,C or G

<400> 130

ccctttttta	tggaatgagt	agactgtatg	tttgaanatt	tanccacaac	ctctttgaca	60
tataatgacg	caacaaaaag	gtgctgttta	gtcctatggt	tcagtttatg	cccctgacaa	120
gtttccattg	tgttttgccg	atctttctggc	taatcggtgt	atcctccatg	ttattagtaa	180
ttctgtattc	cattttgtta	acgcctggta	gatgtaacct	gctangaggc	taactttata	240
cttattttaa	agctcttatt	ttgtgggtcat	taaaatggca	atztatgtgc	agcactttat	300
tgcagcagga	agcacgtgtg	ggttgggtgt	aaagctcttt	gctaattcta	aaaagtaatg	360
gg						362

<210> 131

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 131

ctttttgaaa	gatcgtgtcc	actcctgtgg	acatcttgtt	ttaatggagt	ttcccatgca	60
gtangactgg	tatggttgca	gctgtccaga	taaaaacatt	tgaagagctc	caaaatgaga	120
gttctcccag	gttcgcctcg	ctgctccaag	tctcagcagc	agcctctttt	aggaggcatc	180
ttctgaaacta	gattaaggca	gcttgtaaat	ctgatgtgat	ttgggtttatt	atccaactaa	240
cttccatctg	ttatcaactgg	agaaagccca	gactccccan	gacnggtacg	gattgtgggc	300
atanaaggat	tgggtgaagc	tggcgtttgtg	gt			332

<210> 132

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 132

acttttgcca	ttttgtatat	ataaacaatc	ttgggacatt	ctcctgaaaa	ctaggtgtcc	60
agtggctaag	agaactcgat	ttcaagcaat	tctgaaagga	aaaccagcat	gacacagaat	120
ctcaaattcc	caaacagggg	ctctgtggga	aaaatgaggg	aggacctttg	tatctcgggt	180
tttagcaagt	taaaatgaan	atgacaggaa	aggcttattt	atcaacaaag	agaagagttg	240
ggatgcttct	aaaaaaaaact	ttggtagaga	aaataggaat	gctnaatcct	agggaagcct	300
gtaacaatct	acaattggtc	ca				322

<210> 133

<211> 278

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 133
 acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt 60
 cttgtttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta 120
 ctattttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg 180
 ctatttcctgt tttgtcaaag aaattatatt tttcaaaaata tgtntatttg tttgatgggt 240
 cccacgaaac actaataaaa accacagaga ccagcctg 278

<210> 134
 <211> 121
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(121)
 <223> n = A,T,C or G

<400> 134
 gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca 60
 tgattctctg aggttaaact tggttttcaa atgttatttt tacttgatt ttgcttttg 120
 t 121

<210> 135
 <211> 350
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(350)
 <223> n = A,T,C or G

<400> 135
 acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc 60
 atancaagtg gtgactgggt aagcgtgcga caaaggtcag ctggcacatt acttggtgtgc 120
 aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca 180
 gggtagcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgt 240
 ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag 300
 ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt 350

<210> 136
 <211> 399
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(399)
 <223> n = A,T,C or G

<400> 136
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60
 gctgtgattg tatccgaata ntcctcgtga gaaaagataa tgagatgacg tgagcagcct 120
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgca ttggctctga 180
 cctggcggcc agccagccag ccacaggtgg gcttcttcct tttgtggtga caacnccaag 240
 aaaactgcag aggccagggt tcaggtgtna gtgggtangt gaccataaaa caccaggtgc 300
 tcccaggaac ccgggcaaaag gccatcccca cctacagcca gcatgccac tggcgtgatg 360
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

50

<210> 137
 <211> 165
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(165)
 <223> n = A,T,C or G

<400> 137
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120
 ttggtcgtgc ccactggtgg tcactgtcat tggtgggggtt cctgt 165

<210> 138
 <211> 338
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(338)
 <223> n = A,T,C or G

<400> 138
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gtttaacagcc acatgcccaa 120
 tgctgggcag tctcccatgc cttccacagt gaaagggctt gagaaaaatc acatccaatg 180
 tcatgtgttt ccagccacac caaaaggtgc ttgggggtgga gggctggggg catananggt 240
 cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300
 aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139
 <211> 382
 <212> DNA
 <213> Homo sapien

<400> 139
 gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa 60
 gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccgaa gtgaaggaga 120
 attcaaacag acctcgtcat tcctggtgtg agcctggtcg gctcaccgcc tatcatctgc 180
 atttgcctta ctcaagggtg accggactct ggcccctgat gtctgtagtt tcacaggatg 240
 ccttattttg cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat 300
 gtcagctatg tgccccatcc tccttcatgc cctccctccc tttcctacca ctgctgagt 360
 gcctggaact tgttttaaagt gt 382

<210> 140
 <211> 200
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(200)
 <223> n = A,T,C or G

<400> 140
 accaaanctt ctttctgttg tgttngattt tactataggg gtttngcttn ttctaaanat 60
 acttttccatt taacancttt tgtaaagtgt caggctgcac ttgctccat anaattattg 120
 ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt 180
 atattcagca taaaggagaa 200

<210> 141
 <211> 335
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(335)
 <223> n = A,T,C or G

<400> 141
 actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg 60
 ggggtgtgac taaacttcaa gtcacagact tttatgtgac agattggagc agggtttgtt 120
 atgcatgtag agaaccctaa ctaatttatt aaacaggata gaaacaggct gtctgggtga 180
 aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg 240
 tttttctacc agttcagaga tnggttaatg actanttcca atgggggaaaa agcaagatgg 300
 attcacaac caagtaattt taaacaaaga cactt 335

<210> 142
 <211> 459
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(459)
 <223> n = A,T,C or G

<400> 142
 accaggttaa tattgccaca tatatccttt ccaattgctg gctaaacaga cgtgtattta 60
 ggggtgttta aagacaaccc agcttaatat caagagaaat tgtgacctt catggagtat 120
 ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180
 cacatgtgac aacaacactc aaataataaa tcaaataatna tcagatgcta aagattggtc 240
 ttcaaacatc atagccaatg atgccccgct tgcctataat ctctccgaca taaaaccaca 300
 tcaacacctc agtggccacc aaaccattca gcacagcttc cttaactgtg agctgtttga 360
 agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420
 cagcangggg gggaggaacc agctcaacct tggcgtant 459

<210> 143
 <211> 140
 <212> DNA
 <213> Homo sapien

<400> 143
 acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60
 aaatccaaac agtctctoct agaaaggaat agtgtacca accccaccca tctccctgag 120
 accatccgac ttccctgtgt 140

<210> 144
 <211> 164
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(164)
 <223> n = A,T,C or G

<400> 144

acttcagtaa	caacatacaa	taacaacatt	aagtgtatat	tgccatcttt	gtcattttct	60
atctatacca	ctctcccttc	tgaaaacaan	aatcactanc	caatcactta	tacaaatttg	120
aggcaattaa	tccatatttg	ttttcaataa	ggaaaaaaag	atgt		164

<210> 145
 <211> 303
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 145

acgtagacca	tccaactttg	tatttgtaat	ggcaaacatc	cagnagcaat	tcctaaacaa	60
actggagggt	atttataccc	aattatccca	ttcattaaca	tgccctcctc	ctcaggctat	120
gcaggacagc	tatcataagt	cggcccaggc	atccagatac	taccatttgt	ataaacttca	180
gtagggggagt	ccatccaagt	gacaggtcta	atcaaaggag	gaaatggaac	ataagcccag	240
tagtaaaatn	ttgcttagct	gaaacagcca	caaaagactt	accgccgtgg	tgattaccat	300
caa						303

<210> 146
 <211> 327
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 146

actgcagctc	aattagaagt	ggtctctgac	tttcatcanc	ttctccctgg	gctccatgac	60
actggcctgg	agtgactcat	tgctctgggt	ggttgagaga	gctcctttgc	caacaggcct	120
ccaagtcagg	gctgggattt	gtttcctttc	cacattctag	caacaatatg	ctggccactt	180
cctgaacagg	gaggggtgga	ggagccagca	tggaacaagc	tgccactttc	taaagtagcc	240
agacttgccc	ctgggcctgt	cacacctact	gatgaccttc	tgtgcctgca	ggatggaatg	300
taggggtgag	ctgtgtgact	ctatggt				327

<210> 147
 <211> 173
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(173)
 <223> n = A,T,C or G

<400> 147

acattgtttt	tttgagataa	agcattgana	gagctctcct	taacgtgaca	caatggaagg	60
actggaacac	ataccacat	ctttgttctg	agggataatt	ttctgataaa	gtcttgctgt	120
atattcaagc	acatatgtta	tatattattc	agttocatgt	ttatagccta	ggt	173

<210> 148
 <211> 477
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(477)
 <223> n = A,T,C or G

<400> 148						
acaaccactt	tatctcatcg	aatttttaac	ccaaactcac	tcaactgtgcc	tttctatcct	60
atgggatata	ttatttgatg	ctccatttca	tcacacatat	atgaataata	cactcatact	120
gccctactac	ctgctgcaat	aatcacattc	ccttctctgtc	ctgaccctga	agccattggg	180
gtggctcctag	tggccatcag	tccangcctg	caccttgagc	ccttgagctc	cattgctcac	240
nccancccac	ctcaccgacc	ccatcctctt	acacagctac	ctccttgctc	tctaacccca	300
tagattatnt	ccaaattcag	tcaattaagt	tactattaac	actctaccgg	acatgtccag	360
caccactggg	aagccttctc	cagccaacac	acacacacac	acacncacac	acacacatat	420
ccaggcacag	gctacctcat	cttcacaatc	acccctttta	ttacctgct	atggtgg	477

<210> 149
 <211> 207
 <212> DNA
 <213> Homo sapien

<400> 149						
acagttgtat	tataatatca	agaaataaac	ttgcaatgag	agcattttaag	agggagaagac	60
taacgtat	tagagagcca	aggaagggtt	ctgtgggggag	tgggatgtaa	ggtggggcct	120
gatgataaat	aagagtcagc	caggtaagt	ggtgggtgtg	tatgggcaca	gtgaagaaca	180
tttcaggcag	agggaaacag	agtga				207

<210> 150
 <211> 111
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(111)
 <223> n = A,T,C or G

<400> 150						
accttgattt	cattgctgct	ctgatggaaa	cccaactatc	taatttagct	aaaacatggg	60
cacttaaagt	tggtcagtgt	ttggacttgt	taactantgg	catctttggg	t	111

<210> 151
 <211> 196
 <212> DNA
 <213> Homo sapien

<400> 151						
agcgcggcag	gtcatattga	acattccaga	tacctatcat	tactcgatgc	tgttgataac	60
agcaagatgg	ctttgaactc	agggtcacca	ccagctattg	gaccttacta	tgaaaaccat	120
ggataccaac	cggaaaaccc	ctatcccgca	cagccactg	tggtccccac	tgtctacgag	180

gtgcatccgg ctccagt

196

<210> 152

<211> 132

<212> DNA

<213> Homo sapien

<400> 152

acagcacttt cacatgtaag aagggagaaa ttcctaaatg taggagaaag ataacagAAC	60
cttcccccttt tcatctagt gtggaaacct gatgctttat gttgacagga atagaaccag	120
gagggagttt gt	132

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(285)

<223> n = A,T,C or G

<400> 153

acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag	60
cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga	120
gcacatcaat aaagtccaaa gtcttggact tggccttggc ttggaggaag tcatcaacac	180
cctggctagt gaggggtcgg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca	240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt	285

<210> 154

<211> 333

<212> DNA

<213> Homo sapien

<400> 154

accacagtcc tgttgggcca gggcttcatg accctttctg tgaaaagcca tattatcacc	60
accccaaatt ttcccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac	120
cctaagccgg ttacacagct aactccact ggcctgtatt tgtgaaattg ctgctgcctg	180
attggcacag gagtcgaagg tgttcagctc ccctcctcgg tggaacgaga ctctgatttg	240
agtttcacaa attctcgggc cacctcgtca ttgctcctct gaaataaaat ccggagaatg	300
gtcaggcctg tctcatccat atggatcttc cgg	333

<210> 155

<211> 308

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(308)

<223> n = A,T,C or G

<400> 155

actggaaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg	60
gaaagtgtt ttgggaactgt aaagtgccta acacatgac gatgattttt gttataatat	120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcctcc	180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggt	240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcattgctg	300

gccctggt

308

<210> 156
 <211> 295
 <212> DNA
 <213> Homo sapien

<400> 156
 accttgctcg gtgcttgga catattagga actcaaaata tgagatgata acagtgccta 60
 ttattgatta ctgagagaac tgtagacat ttagttgaag attttctaca caggaactga 120
 gaataggaga ttatgtttgg ccctcatatt ctctcctatc ctccctgcct cattctatgt 180
 ctaatatatt ctcaatcaaa taaggtttagc ataatcagga aatcgaccaa ataccaatat 240
 aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat 295

<210> 157
 <211> 126
 <212> DNA
 <213> Homo sapien

<400> 157
 acaagtttaa atagtgtgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct 60
 gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtogtgggta tatctgtccc 120
 cttagt 126

<210> 158
 <211> 442
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (442)
 <223> n = A,T,C or G

<400> 158
 acccactggt cttggaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60
 aanccagcag gctgccccta gtcagtcctt ccttcacagag aaaaagagat ttgagaaagt 120
 gcctgggtaa ttcaccatta atttcctccc ccaaactctc tgagtcttcc cttaatat 180
 ctggtgggtc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta 240
 natgtttgta gccttgcata cttagccctt. cccacgcaca aacggagtgg cagagtgggtg 300
 ccaacccctgt tttcccgatc cacgtagaca gattcacagt gcggaattct ggaagctgga 360
 nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg 420
 tgttcattct ctgatgtcct gt 442

<210> 159
 <211> 498
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (498)
 <223> n = A,T,C or G

<400> 159
 acttccagggt aacgtttgttg tttccgttga gcctgaactg atgggtgacg ttgtaggttc 60
 tccaacaaga actgaggttg cagagcgggt agggagagat gctgttccag ttgcacctgg 120
 gctgctgtgg actgttgttg attcctcact acggcccaag gttgtggaac tggcanaaag 180

gtgtgttgtt	gganttgagc	tcgggctggc	gtggttaggt	gtgggctctt	caacaggggc	240
tgctgtggg	ccgggangtg	aangtggtgt	gtcacttgag	cttgccagc	tctggaaagt	300
antanattct	tcctgaaggc	cagcgcttgt	ggagctggca	ngggtcantg	ttgtgtgtaa	360
cgaaccagt	ctgtctgtgg	tgggtgtana	tcctccacaa	agcctgaagt	tatgggtcn	420
tcaggtaana	atgtggttct	agtgtccctg	ggcngctgtg	gaagggtgta	nattgtcacc	480
aagggaataa	gctgtggt					498

<210> 160
 <211> 380
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(380)
 <223> n = A,T,C or G

<400> 160						
acctgcatcc	agcttccctg	ccaaactcac	aaggagacat	caacctctag	acagggaaac	60
agcttcagga	tacttccagg	agacagagcc	accagcagca	aaacaaatat	tcccatgcct	120
ggagcatggc	atagaggaag	ctganaaatg	tggggtctga	ggaagccatt	tgagtctggc	180
cactagacat	ctcatcagcc	acttgtgtga	agagatgccc	catgacccca	gatgcctctc	240
ccacccttac	ctccatctca	cacacttgag	ctttccactc	tgtataattc	taacatcctg	300
gagaaaaatg	gcagtttgac	cgaacctgtt	cacaacggtg	gaggctgatt	tctaacgaaa	360
cttgtagaat	gaagcctgga					380

<210> 161
 <211> 114
 <212> DNA
 <213> Homo sapien

<400> 161						
actccacatc	ccctctgagc	aggcggttgt	cgttcaaggt	gtatttggcc	ttgcctgtca	60
cactgtccac	tggcccctta	tccacttggt	gcttaatccc	togaaagagc	atgt	114

<210> 162
 <211> 177
 <212> DNA
 <213> Homo sapien

<400> 162						
actttctgaa	tcgaatcaaa	tgatacttag	tgtagtttta	atatcctcat	atatatcaaa	60
gttttactac	tctgataatt	ttgtaaacca	ggttaaccaga	acatccagtc	atacagcttt	120
tggtgatata	taacttggca	ataaccagct	ctggtgatac	ataaaactac	tcactgt	177

<210> 163
 <211> 137
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(137)
 <223> n = A,T,C or G

<400> 163						
catttatata	gacagcggtg	aagacattca	cgacaaaaac	gcgaaattct	atcccgtgac	60
canagaaggc	agctacggct	actcctacat	cctggcggtg	gtggccttcg	cctgcacctt	120

catcagcggc atgatgt

137

<210> 164
 <211> 469
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (469)
 <223> n = A,T,C or G

<400> 164
 cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta 60
 tgcaatgcat catgctatct catacctaata gagggagttc caggagattc aaccaggaaa 120
 tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt 180
 gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg 240
 ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg 300
 gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct 360
 tctagtaggc acagggtcc caggccaggc ctcattctcc tctggcctct aatagtcaat 420
 gattgtgtag ccatgcctat cagtaaaaaa atntttgagc aaacacttt 469

<210> 165
 <211> 195
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (195)
 <223> n = A,T,C or G

<400> 165
 acagtgtttt atanatatcg acattgccgg cacttggtgtt cagtttcata aagctgggtg 60
 atccgctgtc atccactatt ccttggctag agtaaaaatt attcttatag cccatgtccc 120
 tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact 180
 tcctctgaga tgagt 195

<210> 166
 <211> 383
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (383)
 <223> n = A,T,C or G

<400> 166
 acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc 60
 cgaggtcgga gtccacacca ccggtgtagg tgtgctcaat cttgggcttg gcgcccacct 120
 ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt 180
 ttgcagacc agcctgagca aggggaggat gttcagcttc agctcctctc tcgtcagggtg 240
 gatgccaacc togtctangg tccgtgggaa gctgggtgcc acntcaccta caacctgggc 300
 gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt 360
 nggggccttt ttggtgaact ttc 383

<210> 167

58

<211> 247
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(247)
 <223> n = A,T,C or G

<400> 167

acagagccag	accttggcca	taaatgaanc	agagattaag	actaaacccc	aagtcganat	60
tggagcagaa	actggagcaa	gaagtgggcc	tggggctgaa	gtagagacca	aggccactgc	120
tatanccata	cacagagcca	actctcaggc	caaggcnatg	gttggggcag	anccagagac	180
tcaatctgan	tccaaagtgg	tggtctggaac	actggtcatg	acanaggcag	tgactctgac	240
tgangtc						247

<210> 168
 <211> 273
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(273)
 <223> n = A,T,C or G

<400> 168

acttctaagt	tttctagaag	tggaaggatt	gtantcatcc	tgaaaatggg	tttacttcaa	60
aatccctcan	ccttgttctt	cacnactgtc	tatactgana	gtgtcatgtt	tccacaaagg	120
gctgacacct	gagcctgnat	tttcaatcat	ccctgagaag	ccctttccag	taggggtggg	180
aattcccaac	ttccttgcca	caagcttccc	aggttttctc	ccctggaaaa	ctccagcttg	240
agtcccatgat	acactcatgg	gctgccctgg	gca			273

<210> 169
 <211> 431
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(431)
 <223> n = A,T,C or G

<400> 169

acagccttgg	cttccccaaa	ctccacagtc	tcagtgcaga	aagatcatct	tccagcagtc	60
agctcagacc	aggggtcaaag	gatgtgacat	caacagtttc	tggtttcaga	acaggttcta	120
ctactgtcaa	atgaccccc	atacttcctc	aaaggctgtg	gtaagttttg	cacagggtgag	180
ggcagcagaa	aggggggtant	tactgatgga	caccatcttc	tctgtatact	ccacactgac	240
cttgccatgg	gcaaaggccc	ctaccacaaa	aacaatagga	tcactgctgg	gcaccagctc	300
acgcacatca	ctgacaaccg	ggatggaaaa	agaantgcc	actttcatac	atccaactgg	360
aaagtgatct	gatactggat	tcttaattac	cttcaaaagc	ttctgggggc	catcagctgc	420
tcgaacactg	a					431

<210> 170
 <211> 266
 <212> DNA
 <213> Homo sapien

59

<220>
 <221> misc_feature
 <222> (1)...(266)
 <223> n = A,T,C or G

<400> 170
 acctgtgggc tgggctgtta tgcctgtgcc ggctgctgaa agggagttca gaggtggagc 60
 tcaaggagct ctgcaggcat ttigccaanc ctctccanag canagggagc aacctacact 120
 ccccgctaga aagacaccag attggagtcc tgggagggg agttggggtg ggcatttgat 180
 gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240
 tcaaagctag ggtctggca ggtgga 266

<210> 171
 <211> 1248
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1248)
 <223> n = A,T,C or G

<400> 171
 ggcagccaaa tcataaacgg cgaggactgc agcccgcaact cgcagccctg gcaggcggca 60
 ctgggtcatgg aaaacgaatt gttctgctcg ggcgctcctg tgcacccgca gtgggtgctg 120
 tcagccgcac actgtttcca gaagtgaagt cagagctcct acaccatcgg gctgggcctg 180
 cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240
 cggeaceccag agtacaacag acccttgcct gctaacgacc tcatgctcat caagttggac 300
 gaatecgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360
 gcggggaaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420
 gtgctgcagt gcgtgaacgt gtcggtgggtg tctgaggagg tctgcagtaa gctctatgac 480
 ccgctgtacc accccagcat gttctgcgcc ggccggagggc aagaccagaa ggactcctgc 540
 aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc 600
 ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtc acaccaacct ctgcaaattc 660
 actgagtggg tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720
 attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agcccctcct 780
 ccctcaggcc caggagtcca ggccccagc ccctcctccc tcaaaccaag ggtacagatc 840
 cccagcccc cctccctcag acccaggagt ccagaccccc cagcccctcc tccctcagac 900
 ccaggagtcc agcccctcct ccctcagacc caggagtcca gacccccag cccctcctcc 960
 ctcagaccca ggggtccagg cccccaaccc ctctcctccc agactcagag gtccaagccc 1020
 ccaaccntc attccccaga cccagaggtc cagggtcccag cccctcntcc ctcagaccca 1080
 gcggtccaat gccacctaga ctntccctgt acacagtgcc ccttgtggc acgttgacct 1140
 aacctacca gttggtttt ctttttngt ccctttcccc tagatccaga aataaagttt 1200
 aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1248

<210> 172
 <211> 159
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(159)
 <223> Xaa = Any Amino Acid

<400> 172
 Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1 5 10 15

60

```

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
      20      25      30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
      35      40      45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
      50      55      60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
      65      70      75      80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
      85      90      95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
      100      105      110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
      115      120      125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
      130      135      140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
      145      150      155

```

<210> 173
 <211> 1265
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1265)
 <223> n = A,T,C or G

```

<400> 173
ggcagccccg actcgagcc ctggcaggcg gcactgggtca tggaaaacga attgttctgc      60
tcgggcgctc tgggtgcatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc      120
tacaccatcg ggctgggccc gcacagtctt gaggccgacc aagagccagg gagccagatg      180
gtggaggcca gcctctccgt acggcaccca gagtacaaca gacccttgct cgctaacgac      240
ctcatgtctc tcaagttgga cgaatccgtg tccgagtcgt acaccatccg gagcatcagc      300
attgcttctc agtgccctac cgcggggaac tcttgccctg tttctggctg gggctctgctg      360
gcgaacggtg agctcacggg tgtgtgtctg ccctcttcaa ggaggtcctc tgcccagtcg      420
cgggggctga cccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga      480
acgtgtcggg ggtgtctgag gaggtctgca gtaagctcta tgaccgctg taccacccca      540
gcatgttctg gcgcggcgga gggcaagacc agaaggactc ctgcaacggt gactctgggg      600
ggcccctgat ctgcaacggg tacttgacgg gccttggtgc tttcggaaaa gccccgtgtg      660
gccaagttag cgtgccaggg gtctacacca acctctgcaa attcactgag tggatagaga      720
aaaccgtcca ggccagttaa ctctggggac tgggaaccca tgaaattgac ccccaaatac      780
atcctgcgga aggaattcag gaatatctgt tcccagcccc tcctccctca ggcccaggag      840
tccaggcccc cagcccctcc tccctcaaac caagggtaca gatccccagc ccctcctccc      900
tcagaccagc gaggccagac ccccagcccc ctctccctc agaccagga gtccagcccc      960
tcctcctcca gaccaggag tccagacccc ccagcccctc ctccctcaga cccaggggtt      1020
gaggccccca acccctctc ctccagagtc agaggcccaa gcccccaacc cctcgttccc      1080
cagaccagga ggtnnaggtc ccagcccctc ttccntcaga cccagnggtc caatgccacc      1140
tagattttcc ctgnacacag tgcccccttg tggngangttg acccaacctt accagttggt      1200
ttttcatttt tngtcccttt cccctagatc cagaaataaa gtttaagaga nngncaaaaa      1260
aaaaa                                           1265

```

<210> 174
 <211> 1459
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1459)
 <223> n = A,T,C or G

<400> 174

ggtcagccgc	acactgtttc	cagaagtgag	tgcagagctc	ctacaccatc	gggctggggc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	ggtggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgtct	atcaagttag	180
acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgtctcg	cagtgcctta	240
ccgcggggaa	ctcttgccct	gtttctggct	ggggtctgct	ggcgaacggt	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgccagctc	gcgggggctg	accagagagct	360
ctgcgtccca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngagggtctgc	antaagctct	atgaccgcct	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
caggggaagg	tgagagaagg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgacaa	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaaagg	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcattggggc	tgagggcggt	780
gacctccacc	caatagaaaa	tcctcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtcgattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttgga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaaat	tgttgcaact	ctcctaaaat	ttttctgatg	tgtttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttgttcaag	ggtcaactgt	1080
gtaccagag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aaatcaagac	tctacaaaga	ggctgggcag	ggtggctcat	gcctgtaatc	ccagcacttt	1200
gggaggcgag	gcaggcgagat	cacttgaggt	agggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatgggtggc	aggcgctgtg	1320
aatcccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagagggt	1380
gaagtgagtt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaa					1459

<210> 175
 <211> 1167
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1167)
 <223> n = A,T,C or G

<400> 175

gcgcagccct	ggcaggcggc	actggctcatg	gaaaacgaat	tgttctgctc	gggctgctctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	caactgtttcc	agaactccta	caccatcggg	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	180
ctctccgtac	ggcaccacaga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcatc	240
aagtttgacg	aatccgtgtc	cgagtctgac	accatccgga	gcatcagcat	tgcttcgcag	300
tgccctaccg	cggggaaactc	ttgcctcgtn	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcactg	cgtgaacgtg	tcggtgggtg	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgcgg	gcggagggca	agaccagaag	480
gactcctgca	acggtgactc	tggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
gtgtctttcg	gaaaagcccc	gtgtggccaa	cttggcgtgc	caggtgtcta	caccaacctc	600
tgcaaatcca	ctgagtggat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccccca	aatacatcct	gcggaangaa	ttcaggaata	tctgttccca	720
gccctctctc	cctcaggccc	aggagtccag	gccccagcgc	cctcctccct	caaaccaagg	780
gtacagatcc	ccagccctc	ctccctcaga	cccaggagtc	cagaccccc	agccctcnt	840
ccntcagacc	caggagtcca	gcccctcctc	cntcagacgc	aggagtccag	accccccagc	900

```

ccntcntccg tcagaccag ggggtgcaggc ccccaacccc tcntcctca gagtcagagg 960
tccaagcccc caaccctcg ttcccagac ccagaggtnc aggtcccagc ccctcctccc 1020
tcagaccag cgggtccaatg ccacctagan tntccctgta cacagtgcgc ccttggtggca 1080
ngttgaccga accttaccag ttgggttttc attttttgtc cctttcccct agatccagaa 1140
ataaagtnta agagaagcgc aaaaaaa 1167

```

<210> 176
 <211> 205
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1) ... (205)
 <223> Xaa = Any Amino Acid

```

<400> 176
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1      5      10      15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20     25     30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
35     40     45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
50     55     60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65     70     75     80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
85     90     95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
100    105    110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
115    120    125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
130    135    140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
145    150    155    160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
165    170    175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
180    185    190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
195    200    205

```

<210> 177
 <211> 1119
 <212> DNA
 <213> Homo sapien

```

<400> 177
gcgcactcgc agccctggca ggcggcactg gtcattgaaa acgaattggt ctgctcgggc 60
gtcctgggtg atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctcctacacc 120
atcgggctgg gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag 180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg 240
ctcatcaagt tggacgaatc cgtgtccagag tctgacacca tccggagcat cagcattgct 300
tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctggggtct gctggcgaac 360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420
caaccctggc aggttgttac catttcggca acttccagtg caaggacgtc ctgctgcata 480

```

63

```

ctcactgggt gctcactact gctcactgca tcacccggaa cactgtgata aactagccag 540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc 720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctgggtactc ccctcacaaa 780
ttcatttttc ctgtttagt gaaagggtgc ccctctggag cctcccaggg tgggtgtgca 840
ggtcacaatg atgaatgtat gatcgtgttc ccattacca aagccttta atccctcatg 900
ctcagtacac cagggcagggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca 960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg 1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc 1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaaa 1119

```

<210> 178

<211> 164

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(164)

<223> Xaa = Any Amino Acid

<400> 178

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1      5      10      15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20     25     30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
35     40     45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
50     55     60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65     70     75     80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
85     90     95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100    105    110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115    120    125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130    135    140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Thr Ala Ser
145    150    155    160
Pro Gly Thr Leu

```

<210> 179

<211> 250

<212> DNA

<213> Homo sapien

<400> 179

```

ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
ccagctgccc ccggccgggg gatgcgaggc toggagcacc cttgcccggc tgtgattgct 120
gccaggcact gttcatctca gcttttctgt ccctttgtct ccggcaagcg cttctgctga 180
aagttcatat ctggagcctg atgtcttaac gaataaagggt cccatgctcc acccgaaaaa 240
aaaaaaaaaa

```

64

<210> 180
 <211> 202
 <212> DNA
 <213> Homo sapien

<400> 180
 actagtccag tgtgggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60
 tcacccagac cccgcccctg cccgtgcccc acgctgctgc taacgacagt atgatgctta 120
 ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttggt tataaatgcc 180
 tgatttaaaa aaaaaaaaaa aa 202

<210> 181
 <211> 558
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(558)
 <223> n = A,T,C or G

<400> 181
 tccytttkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg 60
 aatgtttagg cagtgttagt aatttcytcg taatgattct gttattactt tcctnattct 120
 ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa 180
 ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca 240
 aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac 300
 ctactctgtt ccttggctag aaaaaattat aaacaggact ttgttagttt gggaagccaa 360
 attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw 420
 ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt 480
 aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc 540
 caaaaaaaaa aaaaaaaaaa 558

<210> 182
 <211> 479
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(479)
 <223> n = A,T,C or G

<400> 182
 acagggwttk grggatgcta agsccccrga rwtggtttga tccaaccctg gcttwttttc 60
 agaggggaaa atggggccta gaagttacag mscatytagy tgggtgcgmg gcacccctgg 120
 cstcacacag astcccagat agctgggact acaggcacac agtcactgaa gcaggccctg 180
 ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca 240
 ctaagggttaa actttccac ccagaaaagg caacttagat aaaatcttag agtactttca 300
 tactmttcta agtcctcttc cagcctcact kkgagtcctm cytgggggtt gataggaant 360
 ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg tacgcatara 420
 awtgstgara aaattaaaat gttctggtty mactttaaaa aaaaaaaaaa aaaaaaaaaa 479

<210> 183
 <211> 384
 <212> DNA
 <213> Homo sapien

<400> 183
 aggcgggagc agaagctaaa gccaaagccc aagaagagtgc gcagtgccag cactggtgcc 60
 agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgtc 120
 ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt 180
 gccagcacca gtggcagctc tgggtgcctgt ggtttctcct acaagtgaga ttttagatat 240
 tgtaaatcct gccagtcttt ctcttcaagc caggggtgcat cctcagaaac ctactcaaca 300
 cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt 360
 gccatttcaa aaaaaaaaaa aaaa 384

<210> 184
 <211> 496
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(496)
 <223> n = A,T,C or G

<400> 184
 accgaattgg gaccgctggc ttataagcga tcatgttynt ccrgtatcac ctcaacgagc 60
 agggagatcg agtctatacg ctgaagaaat ttgaccgat gggacaacag acctgctcag 120
 cccatcctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga 180
 aacgcttcaa ggtgctcatg acccagcaac cgcgcctgt cctctgaggg tcccttaaac 240
 tgatgtcttt tctgccacct gttaccacct ggagactccg taaccaaaact cttcggactg 300
 tgagccctga tgcctttttg ccagccatac tctttggcat ccagtctctc gtggcgattg 360
 attatgcttg tgtgaggcaa tcatggtggc atcaccata aagggaacac atttgacttt 420
 tttttctcat attttaaat actacmagaw tattwmagaw waaatgawtt gaaaaactst 480
 taaaaaaaaa aaaaaa 496

<210> 185
 <211> 384
 <212> DNA
 <213> Homo sapien

<400> 185
 gctggtagcc tatggcgkgg ccacgaggg ggtcctgag gccacggrac agtgacttcc 60
 caagtatcyt ggcsgcgtc ttctaccgtc cctacctgca gatcttcggg cagattcccc 120
 aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggcttct 180
 ggacacaccc tctgggggcc caggcgggca cctgcgtctc ccagtatgcc aactggctgg 240
 tgggtgctgct cctcgtcatc ttctgctcg tggccaacat cctgctggtc aacttgctca 300
 ttgccatgtt cagttacaca ttcggcaaag tacagggcaa cagcgatctc tactgggaag 360
 gcgcagcgtt accgcctcat ccgg 384

<210> 186
 <211> 577
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(577)
 <223> n = A,T,C or G

<400> 186
 gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc 60
 tnccatcgtc atactgtagg tttgccacca cytcttgcca tcttggggcg gcntaatatt 120
 ccaggaaact ctcaatcaag tcaccgtcga tgaaacctgt gggctgggtc tgtcttcgcg 180

tcggtgtgaa	aggatctccc	agaaggagt	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtagcag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mcgtgccgaa	garcaccgag	ccttggtgtg	gggkkgag	360
ctcaccacga	ttctgcatta	ccagagagcc	gtggcaaaa	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttggt	ggcagcgctw	480
tccttttgac	acacaaacaa	gttaaaggca	ttttcagccc	ccagaaaant	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

<210> 187
 <211> 534
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(534)
 <223> n = A,T,C or G

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctggatttaa	aattcacaa	atgcaacact	120
ttaaaccagt	tgtcaatctg	ctcccynac	tttgtcatca	ccagtctggg	aakaagggtg	180
tgccctattc	acacctgtta	aaagggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatgggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttygggagc	360
tgatatttga	gcggaagagt	agcctttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgtcttg	480
aggatctccc	agtttatatta	ccacttgcac	aagaaggcgt	tttcttcttc	aggc	534

<210> 188
 <211> 761
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(761)
 <223> n = A,T,C or G

agaaaccagt	atctctnaaa	acaacctctc	ataccttggt	gacctaat	ttgtgtcggt	60
ttgtgtgtgc	cgcatattat	atagacaggc	acatcttttt	tactttttgt	aaagcttatg	120
cctcttttgg	atctatatct	gtgaaagt	taatgatctg	ccataatgtc	ttggggacct	180
ttgtcttctg	tgtaaatggt	actagagaaa	acacctatnt	tatgagtcaa	tctagttngt	240
tttattcgac	atgaaggaaa	tttccagatn	acaacactna	caaactctcc	ctkgackarg	300
ggggacaaa	aaaagcaaaa	ctgamcataa	raaacaatwa	cctgggtgaga	arttgcataa	360
acagaaatwr	ggtagtatat	tgaarnacag	catcattaaa	rmgttwtktt	wttctccott	420
gcaaaaaaca	tgtacngact	tcccgttgag	taatgccaa	ttgttttttt	tatnataaaa	480
cttgcccttc	attacatggt	tnaaagtgg	gtgggtggcc	aaaatattga	aatgatggaa	540
ctgactgata	aagctgtaca	aataagcagt	gtgcctaaca	agcaacacag	taatgttgac	600
atgcttaatt	cacaaatgct	aatttcatta	taaagtgttg	ctaaaatata	ctttgaacta	660
tttttctgtn	ttcccagagc	tgagatntta	gattttatgt	agtatnaagt	gaaaaantac	720
gaaaataata	acattgaaga	aaaananaaa	aaanaaaaaa	a		761

<210> 189
 <211> 482
 <212> DNA
 <213> Homo sapien

67

<220>
 <221> misc_feature
 <222> (1)...(482)
 <223> n = A,T,C or G

<400> 189
 tttttttttt ttgtccgatn ctactatattt attgcaggan gtgggggtgt atgcaccgca 60
 caccgggggt atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca 120
 aagccgcctg ctgccttctc tgtctgtctc ctgggtcagg cacatgggga gaccttcccc 180
 aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggagtgt gcataagaag 240
 tgataggcac aggccacccg gtacagaccc ctccggctcct gacaggtnga tttcgaccag 300
 gtcattgtgc cctgccagg cacagcgtan atctggaaaa gacagaatgc tttccttttc 360
 aaatttggct ngtcattngaa ngggcanttt tccaanttn gctnggtctt ggtacncttg 420
 gttcggccca gtcctcgtc caaaaantat tcaccnct ccnaattgct tgcnggnccc 480
 cc 482

<210> 190
 <211> 471
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(471)
 <223> n = A,T,C or G

<400> 190
 tttttttttt tttfaaaaca gtttttcaca acaaaattta ttagaagaat agtggttttg 60
 aaaactctcg catccagtga gaactacat acaccacatt acagctngga atgtntctca 120
 aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag 180
 cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt 240
 taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt 300
 tgaaaaattt catgtatgca atccaaccaa agaacttnat tggatgatcat gantnctcta 360
 ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacncngt acaaaaaanaa 420
 tctgtaattn anttcaacct ccgtacngaa aaatntntnt tatacactcc c 471

<210> 191
 <211> 402
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(402)
 <223> n = A,T,C or G

<400> 191
 gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct 60
 gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa 120
 attcttcacc agtcacatct tctaggacct ttttggattc agttagtata agctcttcca 180
 cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg 240
 ctctgtctct aacaatgtcc tctccttgaa gtatttggct gaacaacca cctaaagtcc 300
 ctttgtgcat ccatttttaa tatacttaat agggcattgk tncactaggt taaattctgc 360
 aagagtcatc tgtctgcaaa agttgcgtta gtatatctgc ca 402

<210> 192
 <211> 601

68

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(601)
 <223> n = A,T,C or G

<400> 192
 gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact 60
 ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac 120
 atgcytyttt gaytaccgtg tgccaagtgc tgggtattct yaacacacyt ccatcccgyt 180
 cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcacc 240
 acgagacact tgaaaggtgt aacaaagcga ytcttgcatt gctttttgtc cctccggcac 300
 cagttgtcaa tactaaccgg ctggtttgcc tccatcacat ttgtgatctg tagctctgga 360
 tacatctcct gacagtactg aagaacttct tctttgtt caaaagcarg tcttggtgcc 420
 tggttgatca gggtccatt tcccagtcyg aatgttcaca tggcatattt wacttcccac 480
 aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag 540
 cctcgatgta gccggccagc gccaaaggcag gcgccgtgag ccccaccagc agcagaagca 600
 g 601

<210> 193
 <211> 608
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(608)
 <223> n = A,T,C or G

<400> 193
 atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact 60
 ggtcccgtg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcytt 120
 cccaacgcag gcagmagcgg gscgggtcaa tgaactccay tcgtggcttg gggtkgacgg 180
 tkaagtgcag gaagaggctg accacctcgc ggtccaccag gatgcccgac tgtgcgggac 240
 ctgcagcgaa actcctcgat ggtcatgagc gggaagcgaa tgaggcccag ggccttgccc 300
 agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctcggcctcg 360
 gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgtcgcgctc 420
 caggammgsc accagcgtgt ccaggtcaat gtcggtgaag ccctccgcgg gtratggcgt 480
 ctgcagtgtt tttgtcgatg ttctccaggc acaggctggc cagctgcggt tcatcgaaga 540
 gtcgcgcctg cgtgagcagc atgaaggcgt tgtcggctcg cagttcttct tcaggaactc 600
 cacgcaat 608

<210> 194
 <211> 392
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 194
 gaacggctgg accttgccctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt 60
 ccagtccgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc 120
 tccgcctcaa tgcagaacca gtagtgggag cactgtgttt agagttaaga gtgaacactg 180

tttgatttta	cttggaatt	tcctctgtta	tatagctttt	cccaatgcta	atttccaaac	240
aacaacaaca	aaataacatg	tttgctgtt	aagttgtata	aaagtaggtg	attctgtatt	300
taaagaaaat	attactgtta	catatactgc	ttgcaatttc	tgtattttatt	gktnctstgg	360
aaataaatat	agttattaaa	ggttgtcant	cc			392

<210> 195
 <211> 502
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(502)
 <223> n = A,T,C or G

<400> 195						
ccsttkgagg	ggtkaggkyc	cagttyccga	gtggaagaaa	caggccagga	gaagtgcgtg	60
ccgagctgag	gcagatgttc	ccacagtgc	ccccagagcc	stgggstata	gtytctgacc	120
cctcncaagg	aaagaccacs	ttctggggac	atgggctgga	gggcaggacc	tagaggcacc	180
aaggaaggc	cccattccgg	ggstgttccc	cgaggaggaa	gggaaggggc	tctgtgtgcc	240
ccccasgagg	aagaggccct	gagtcctggg	atcagacacc	ccttcacgtg	tatccccaca	300
caaagtcaag	ctcaccaagg	tcccctctca	gtccccttcc	stacaccctg	amcggccact	360
gscscacacc	caccagagc	acgccaccog	ccatggggar	tgtgctcaag	gartcgcnng	420
gcarcgtgga	catctngtcc	cagaaggggg	cagaatctcc	aatagangga	ctgarcmstt	480
gctnanaaaa	aaaaanaaaa	aa				502

<210> 196
 <211> 665
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(665)
 <223> n = A,T,C or G

<400> 196						
ggttacttgg	tttctattgc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgccgag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	120
wagctgtttk	gagttgatts	gcaccactgc	accacaaact	tcaatatgaa	aacyawttga	180
actwatattat	tatcttgtga	aaagtataac	aatgaaaatt	ttgttcatac	tgtattkatc	240
aagtatgatg	aaaagcaawa	gatatatatt	cttttattat	gttaaattat	gattgccatt	300
attaatcggc	aaaatgtgga	gtgtatgttc	ttttcacagt	aatatatgcc	ttttgtaact	360
tcacttgggt	attttattgt	aaatgartta	caaaattctt	aatttaagar	aatggatatg	420
watattttatt	tcattaattt	ctttcctkgt	ttacgtwaat	tttgaaaaga	wtgcatgatt	480
tcttgacaga	aatcgatctt	gatgctgtgg	aagtagtttg	accacatcc	ctatgagttt	540
ttcttagaat	gtataaagg	tgtagcccat	cnaacttcaa	agaaaaaat	gaccacatac	600
tttgcaatca	ggctgaaatg	tggcatgctn	ttctaattcc	aactttataa	actagcaaan	660
aagtg						665

<210> 197
 <211> 492
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(492)

<223> n = A,T,C or G

<400> 197

ttttnttttt	ttttttttgc	aggaaggatt	ccattttattg	tggatgcatt	ttcacaatat	60
atgtttattg	gagcgatcca	ttatcagtga	aaagtatcaa	gtgtttataa	natttttagg	120
aaggcagatt	cacagaacat	gctngtcngc	ttgcagtttt	acctcgta	gatnacagag	180
aattatagtc	naaccagtaa	acnaggaatt	tacttttcaa	aagattaaat	ccaaactgaa	240
caaaattcta	ccctgaaact	tactccatcc	aaatattgga	ataanagtca	gcagtgtac	300
attctcttct	gaactttaga	ttttctagaa	aaatattgta	tagtgatcag	gaagagctct	360
tgttcaaaag	tacaacnaag	caatgttccc	ttaccatagg	ccttaattca	aactttgatc	420
catttcactc	ccatcacggg	agtcaatgct	acctgggaca	cttgatattt	gttcatnctg	480
ancntggctt	aa					492

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(478)

<223> n = A,T,C or G

<400> 198

ttnttttgn	atttcantct	gtannaanta	ttttcattat	gtttattana	aaaatatnaa	60
tgtntccacn	acaaatcatn	ttacntnagt	aagaggccan	ctacattgta	caacatacac	120
tgagtatat	ttgaaaagga	caagtttaaa	gtanacncat	attgccganc	atancacatt	180
tatacatggc	ttgattgata	tttagcacag	canaaactga	gtgagttacc	agaaanaaat	240
nataatgtgc	aatcngattt	aagatacaaa	acagatccta	tggtacatan	catcntgtag	300
gagttgtggc	tttatgttta	ctgaaagtca	atgcagttcc	tgtacaaaga	gatggccgta	360
agcattctag	tacctctact	ccatgggtta	gaatcgtaca	cttatgttta	catatgtnc	420
gggtaagaat	tgtgttaagt	naanttatgg	agaggccan	gagaaaaatt	tgatncaa	478

<210> 199

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 199

agtgacttgt	cctccaacaa	aacccttga	tcaagtttgt	ggcactgaca	atcagaccta	60
tgctagtcc	tgtcatctat	tcgctactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaactctatt	cctacttgta	cggactttga	180
agtgatccag	tttctcttac	ggatgagaga	ctggctcaag	aatatcctca	tcagacttta	240
tgaagccnac	tctgaacacg	ctggttatct	nagatgagaa	ncagagaaat	aaagtcnaga	300
aaatttacct	ggangaaaag	aggctttngg	ctggggacca	tcccattgaa	ccttctctta	360
anggacttta	agaanaaaact	accacatgtn	tgtngtatcc	tggtgccngg	ccgtttantg	420
aacntngacn	ncacccttnt	ggaatanant	cttgacngcn	tcctgaactt	gctcctctgc	480
ga						482

<210> 200

<211> 270

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(270)
 <223> n = A,T,C or G

<400> 200
 cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc 60
 cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc 120
 aaggctgagc tgacgccgca gaggtcgtgt cacgtccac gacctgacg ccgtcgggga 180
 cagccggaac agagcccggt gaangcggga ggcctcggg agcccctcgg gaaggcgggc 240
 ccgagagata cgcaggtgca ggtggccgcc 270

<210> 201
 <211> 419
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(419)
 <223> n = A,T,C or G

<400> 201
 tttttttttt ttttggaaac tactgcgagc acagcaggtc agcaacaagt ttatttttgca 60
 gctagcaagg taacagggtta gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg 120
 ttgattggtt tgtctttatg ggggcggggt ggggtagggg aaancgaagc anaantaaca 180
 tggagtgggt gcacctccc tgtagaacct gggtacnaaa gcttggggca gttcacctgg 240
 tctgtgaccg tcatttttctt gacateaatg ttattagaag tcaggatata ttttagagag 300
 tccactgtnt ctggaggag attaggggtt cttgccana tccaancaa atccacntga 360
 aaaagttgga tgatncangt acngaatacc ganggcatan ttctcatant cggtgggcca 419

<210> 202
 <211> 509
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(509)
 <223> n = A,T,C or G

<400> 202
 tttntttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
 tggcacttaa tccattttta tttcaaaatg tctacaaant ttnaatncnc cattatacng 120
 gtnattttnc aaaaatctaaa nnttattcaa atntnagcca aantccttac ncaaatnnaa 180
 tacnncnaaa aatcaaaaat atacntntct ttcagcaaac ttngttacat aaattaaaaa 240
 aatatatacg gctggtgttt tcaaagtaca attatcttaa cactgcaaac atnttttnaa 300
 ggaactaaaa taaaaaaaaa cactnccgca aagggttaaag ggaacaacaa attcntttta 360
 caacancnnc nattataaaa atcatatctc aaatcttagg ggaatatata cttcacacng 420
 ggatcttaac ttttactnca ctttgtttat ttttttanaa ccattgtntt gggcccaaca 480
 caatggnaat nccnccnccncc tggactagt 509

<210> 203
 <211> 583
 <212> DNA
 <213> Homo sapien

72

<220>
 <221> misc_feature
 <222> (1)... (583)
 <223> n = A,T,C or G

<400> 203

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaagtggaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaaatcttc	tctagctctt	ttgactgtaa	attttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaactc	ttccattttt	tccctattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaca	ggaagagana	atggcacaca	aaacaaacat	tttatattca	tatttctacc	420
tacgttaata	aaatagcatt	ttgtgaagcc	agctcaaaag	aaggccttaga	tccttttatg	480
tcatttttag	tcactaaacg	atatcnaaag	tgccagaatg	caaaagggtt	gtgaacattt	540
attcaaaagc	taatataaga	tatttcacat	actcatcttt	ctg		583

<210> 204
 <211> 589
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (589)
 <223> n = A,T,C or G

<400> 204

ttttttttnt	tttttttttt	tttttttctc	ttcttttttt	ttganaatga	ggatcgagtt	60
tttcaactctc	tagatagggc	atgaagaaaa	ctcatctttc	cagcttttaa	ataacaatca	120
aatctcttat	gctatatcat	atttttaagtt	aaactaatga	gtcactggct	tatcttctcc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagagggtt	ttcttctcta	tttacacata	tatttccatg	tgaatttgta	tcaaaccctt	300
attttcatgc	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaa	tgtttgtaa	gnttatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacatttac	ngacnagcaa	taataaaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tgttattatt	ccntagccca	acacaatgg		589

<210> 205
 <211> 545
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (545)
 <223> n = A,T,C or G

<400> 205

tttttntttt	ttttttcagt	aataatcaga	acaatattta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacatta	agtaaattat	180
ttaagatcat	agagcttgta	agtgaagaaa	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tatttagcaa	taaattacta	tggacttctt	gctttaattt	tgtgatgaat	300
atgggggtgc	actggtaa	caacacattc	tgaaggatac	attacttagt	gatagattct	360
tatgtacttt	gctanaatnac	gtggatatga	gttgacaagt	ttctctttct	tcaatctttt	420
aaggggcnag	ngaaatgagg	aagaaaagaa	aaggattacg	catactgttc	tttctatngg	480

aaggattaga tatgtttcct ttgccaatat taaaaaata ataatgttta ctactagtga 540
aaccc 545

<210> 206
<211> 487
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(487)
<223> n = A,T,C or G

<400> 206
tttttttttt ttttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt 60
catttattag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna 120
caatttataa atgtaagggtg ccattattga gtanatatat tcctccaaga gtggatgtgt 180
cccttctccc accaactaat gaancagcaa cattagttta attttattag tagatnatac 240
actgtgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag 300
ttgtnagaa tgcatacanca atctnacaat caacagcaag atgaagctag gcntgggctt 360
tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cgggtggcaag 420
aactcttcga accgcttcct caaaggcngc tgccacattt gtggcntctn ttgcacttgt 480
ttcaaaa 487

<210> 207
<211> 332
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(332)
<223> n = A,T,C or G

<400> 207
tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa 60
tacatagcat taaatcccaa atoctattta aagacctgac agcttgagaa ggtcactact 120
gcattttatag gaccttctgg tggttctgct gttacntttg aantctgaca atccttgana 180
atctttgcat gcagaggagg taaaagggtat tggattttca cagaggaana acacagcgca 240
gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg 300
aaaagaaggc agcctaggcc ctggggagcc ca 332

<210> 208
<211> 524
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(524)
<223> n = A,T,C or G

<400> 208
agggcggtgt gcggaggggc ttactgtttt gtctcagtaa caataaatac aaaaagactg 60
gttgtgttcc ggccccatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat 120
tttaaaggac atggagcttg tcacaatgtc acaatgtcac agtgtgaagg gcacactcac 180
tcccgcgtga ttcacattta gcaaccaaca atagctcatg agtccatact tgtaaaatac 240
tttggcagaa tacttnttga aacttgacga tgataactaa gatccaagat atttcccaaa 300

gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagcccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgtcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcfaat	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

<210> 209

<211> 159

<212> DNA

<213> Homo sapien

<400> 209

gggtgaggaa	atccagagtt	gcatggaga	aaattccagt	gtcagcattc	ttgtctcttg	60
tggccctctc	ctacactctg	gccagagata	ccacagtcaa	acctggagcc	aaaaaggaca	120
caaaggactc	tcgaccctaa	ctgccccaga	ccctctcca			159

<210> 210

<211> 256

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(256)

<223> n = A,T,C or G

<400> 210

actccctggc	agacaaaggc	agaggagaga	gctctgttag	ttctgtgttg	ttgaactgcc	60
actgaatttc	tttccacttg	gactattaca	tgccanttga	gggactaatg	gaaaaacgta	120
tggggagatt	ttanccaatt	tangtntgta	aatggggaga	ctggggcagg	cgggagagat	180
ttgcagggtg	naaatgggan	ggctgggttg	ttanatgaac	agggacatag	gaggtaggca	240
ccaggatgct	aatca					256

<210> 211

<211> 264

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(264)

<223> n = A,T,C or G

<400> 211

acattgtttt	tttgagataa	agcattgaga	gagctctcct	taacgtgaca	caatggaagg	60
actggaacac	ataccacat	ctttgttctg	agggataatt	ttctgataaa	gtcttgctgt	120
atattcaagc	acatatgtta	tatattattc	agttccatgt	ttatagccta	gttaaggaga	180
ggggagatac	attcngaaag	aggactgaaa	gaaataactca	agtnggaaaa	cagaaaaaga	240
aaaaaaggag	caaatgagaa	gcct				264

<210> 212

<211> 328

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(328)

<223> n = A,T,C or G

<400> 212
 acccaaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa 60
 ggatttaaatg ttgtctcagc ttgggcaqtt cagttaggac ctaaggatgc cagccggcag 120
 gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccggcag 180
 ttnaattttca ttccatttga cttgggatcc ttatcatcag ccagagagat tgaaaattta 240
 ccctacnac tctttactct ctgganaggg ccagtgtgtg tagctataag cttggccaca 300
 ttttttttcc ctttattcct ttgtcaga 328

<210> 213
 <211> 250
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(250)
 <223> n = A,T,C or G

<400> 213
 acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt 60
 taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct 120
 cattatgcca aagganatat acatttcaat tctccaaact tcttctcat tccaagagtt 180
 ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatatc tctctnacct 240
 tctcatcggt 250

<210> 214
 <211> 444
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(444)
 <223> n = A,T,C or G

<400> 214
 acccagaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag 60
 gatttaaatgt tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg 120
 tttatatatg cagcaacaat attcaagcgc gacaacaggc tattgaactt gcccgccagt 180
 tgaatttcat tccattgac ttgggatcct tatcatcagc canagagatt gaaaatttac 240
 ccctacgact ctttactctc tggagagggc cagtgtgtgt agctataagc ttggccacat 300
 ttttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag 360
 agtgactttt acaaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt 420
 actttgtctc ccctaataata cctc 444

<210> 215
 <211> 366
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(366)
 <223> n = A,T,C or G

<400> 215
 acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt 60

taaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgcc	aagganatat	acattttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatattt	gcatgaacct	gctgataagc	catgttgaga	aacaaatata	tctctgacct	240
tctcatcggt	aagcagaggc	tgtaggcaac	atggaccata	gcgaanaaaa	aacttagtaa	300
tccaagctgt	tttctacact	gtaaccaggt	ttccaaccaa	ggtggaaatc	tcctatactt	360
ggtgcc						366

<210> 216
 <211> 260
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(260)
 <223> n = A,T,C or G

<400> 216	
ctgtataaac	agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgctc 60
caagacaggg	gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120
taataaaaag	tnnaaaaggc ctctttctcaa cttttttccc ttnggctgga aaatttaaaa 180
atcaaaaatt	tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240
aattcttcct	tcctctcttt 260

<210> 217
 <211> 262
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 217	
acctacgtgg	gtaagttttan aaatgtttata atttcaggaa naggaacgca tataattgta 60
tcttgcttat	aattttctat tttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120
ggcattctac	agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180
atgaataatc	tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240
atataccttca	tgcttgtaaa gt 262

<210> 218
 <211> 205
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(205)
 <223> n = A,T,C or G

<400> 218	
accaaggtgg	tgcattaccg gaantggatc aangacacca tctgtggccaa cccctgagca 60
cccctatcaa	ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120
aggcctccc	agttctactg acctttgtcc ttangtntna ngtccagggt tgctaggaaa 180
anaaatcagc	agacacagggt gtaaa 205

<210> 219

77

<211> 114
 <212> DNA
 <213> Homo sapien

<400> 219
 tactgttttg tctcagtaac aataaataca aaaagactgg ttgtgttccg gccccatcca 60
 accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
 <211> 93
 <212> DNA
 <213> Homo sapien

<400> 220
 actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta 60
 aaataagcat ttagtgctca gtccttactg agt 93

<210> 221
 <211> 167
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(167)
 <223> n = A,T,C or G

<400> 221
 actangtgca ggtgcgacaca aatatttgtc gatattccct tcatcttgga ttccatgagg 60
 tcttttgccc agcctgtggc tctactgtag taagttttctg ctgatgagga gccagnatgc 120
 cccccactac cttccctgac gtcctccana aatcacccaa cctctgt 167

<210> 222
 <211> 351
 <212> DNA
 <213> Homo sapien

<400> 222
 agggcggtgt gcggaggcg gtactgacct cattagtagg aggatgcatt ctggcaccoc 60
 gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa 120
 atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180
 ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240
 taggtgagca tgattagaga gcttgtaggt tgcttttaca tatatctggc atatttgagt 300
 ctcgatatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t 351

<210> 223
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 223
 aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat 60
 tggttaattat ggtcaattta atwrtrttkt ggggcatttc ottacattgt cttgacaaga 120

78

ttaaaatgtc	tgtgccaaaa	ttttgtat	tatttgaga	cttcttatca	aaagtaatgc	180
tgccaaagga	agtctaagga	attagtagtg	ttcccmccac	ttgtttgag	tgtgctat	240
taaaagattt	tgatttcctg	gaatgacaat	tatatattta	ctttggtggg	ggaaanagtt	300
ataggaccac	agtcttcact	tctgatactt	gtaaattaat	cttttattgc	acttgttttg	360
accattaagc	tatatgttta	aaa				383

<210> 224

<211> 320

<212> DNA

<213> Homo sapien

<400> 224

cccctgaagg	cttcttggtta	gaaaatagta	cagttacaac	caataggaac	aacaaaaaga	60
aaaagtttgt	gacattgtag	tagggagtgt	gtacccctta	ctcccatca	aaaaaaaaat	120
ggatacatgg	ttaaaggata	raagggcaat	atttatcat	atgttctaaa	agagaaggaa	180
gagaaaatac	tactttctcr	aaatggaagc	ccttaaaagt	gctttgatac	tgaaggacac	240
aaatgtggcc	gtccatcctc	ctttaragtt	gcattgacttg	gacacggtaa	ctgttgacgt	300
tttaractcm	gcattgtgac					320

<210> 225

<211> 1214

<212> DNA

<213> Homo sapien

<400> 225

gaggactgca	gcccgcactc	gcagccctgg	caggcgccac	tggtcatgga	aaacgaattg	60
ttctgctcgg	gcgtccctgg	gcatccgcag	tgggtgctgt	cagccgcaca	ctgtttccag	120
aactcctaca	ccatcggtgt	gggcctgcac	agtcttgagg	ccgaccaaga	gccagggagc	180
cagatggtgg	agccagcct	ctccgtacgg	cacccagagt	acaacagacc	cttgctcgct	240
aacgacctca	tgctcatcaa	gttgagacaa	tccgtgtccg	agtctgacac	catccggagc	300
atcagcattg	cttcgcagtg	ccctaccgcg	gggaactcct	gcctogtttc	tggtctgggt	360
ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	tgaacgtgtc	ggtggtgtct	420
gaggaggtct	gcagtaagct	ctatgaccgg	ctgtaccacc	ccagcatggt	ctgcgcgggc	480
ggaggggcaag	accagaagga	ctcctgcaac	ggtgactctg	ggggggccct	gatctgcaac	540
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ggtgtctaca	ccaacctctg	caaattcact	gagtgatag	agaaaaccgt	ccaggccagt	660
taactctggg	gactgggaac	ccatgaaatt	gacccccaaa	tacatcctgc	ggaaggaatt	720
caggaatatc	tggtcccagc	ccctcctccc	tcaggccag	gagtcagggc	ccccagcccc	780
tcctccctca	aaccaagggt	acagatcccc	agccctcct	ccctcagacc	caggagtcca	840
gacccccccag	cccctcctcc	ctcagaccca	ggagtccagc	ccctcctccc	tcagaccag	900
gagtcacagac	ccccagcccc	ctcctcctcc	agaccaggg	gtccaggccc	ccaacccctc	960
ctccctcaga	ctcagaggtc	caagccccca	acccctcctt	ccccagaccc	agaggtccag	1020
gtcccagccc	ctcctccctc	agaccagcg	gtccaatgcc	acctagactc	tccctgtaca	1080
cagtgcctcc	ttgtggcacg	ttgacccaac	cttaccagtt	ggtttttcat	tttttgtccc	1140
tttcccctag	atccagaaat	aaagtctaag	agaagcgcaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa	aaaaa					1214

<210> 226

<211> 119

<212> DNA

<213> Homo sapien

<400> 226

accagtatg	tgcagggaga	cggaacccca	tgtgacagcc	cactccacca	gggttcccaa	60
agaacctggc	ccagtcataa	tcattcatcc	tgacagtggc	aataatcacg	ataaccagt	119

<210> 227

<211> 818

<212> DNA

<213> Homo sapien

<400> 227

acaattcata	gggacgacca	atgaggacag	ggaatgaacc	cggtctctccc	ccagccctga	60
tttttgctac	atatggggtc	ccttttcatt	ctttgcaaaa	acactgggtt	ttctgagaac	120
acggacggtt	cttagcacia	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcctc	ctctggagga	aagggtggtg	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgtcccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttcct	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaagggtg	caccctcagc	agagaagccg	agagcttaac	tctggtcgtt	tccagagaca	480
acctgctggc	tgtcttggtg	tgcgcccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcatgagagg	600
gacaggctct	gccctcaagc	cggtctgagg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggct	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

<210> 228

<211> 744

<212> DNA

<213> Homo sapien

<400> 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccaggtctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaacga	gcctcctcct	tggaagatgg	aagaccgtgt	120
tcgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcggagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcactgt	ggaactacca	aatggcgaga	240
tgctcgggtg	acattggggt	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtcc	acctctgcag	360
gctggcagct	gaatggcttg	ccggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	ggttgctcct	tccaggttgg	480
ccagacggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctggtga	cagtgaaccg	540
ccgtggatat	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttgggggttg	600
ttcttttctg	taatgttcct	ctgtgttgct	agctgtcttc	atttctctgg	ctaagcagca	660
ttgggagatg	tggaaccagag	atccactcct	taagaaccag	tggcgaaaga	cactttcttt	720
cttcaactctg	aagtagctgg	tggt				744

<210> 229

<211> 300

<212> DNA

<213> Homo sapien

<400> 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcattgtgaac	60
cattacacat	cgaaataaaa	gaaaggtggc	agacttgccc	aacgccaggc	tgacatgtgc	120
tgcagggttg	ttgtttttta	attattattg	ttagaaacgt	caccacagct	ccctgttaat	180
ttgtatgtga	cagccaactc	tgagaaggtc	ctatttttcc	acctgcagag	gatccagctc	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

<210> 230

<211> 301

<212> DNA

<213> Homo sapien

<400> 230

cagcagaaca	aatacaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
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80

gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120
caatataaag	tcctgggttca	cactcaggaa	cgagagctga	cccagttaag	ggagaagttg	180
cggaagggga	gagatgcctc	cctctcattg	aatgagcctc	tccaggccct	cctcactccg	240
gatgaaccgg	acaagtccca	ggggcaggac	ctccaagaaa	cagacctcgg	ccgcgaccac	300
g						301

<210> 231
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 231						
gcaagcacgc	tggcaaatct	ctgtcaggtc	agctccagag	aagccattag	tcatttttagc	60
caggaactcc	aagtccacat	ccttggcaac	tggggacttg	cgcaggttag	ccttgaggat	120
ggcaacacgg	gactttctcat	caggaagtgg	gatgtagatg	agctgatcaa	gacggccagg	180
tctgaggatg	gcaggatcaa	tgatgtcagg	ccggttggtta	ccgccaatga	tgaacacatt	240
tttttttgtg	gacatgccat	ccattttctgt	caggatctgg	ttgatgactc	ggtcagcagc	300
c						301

<210> 232
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 232						
agtaggtatt	tcgtgagaag	ttcaacacca	aaactggaac	atagttctcc	ttcaagtgtt	60
ggcgacacgg	gggttctctg	attctggaat	ataactttgt	gtaaattaac	agccacctat	120
agaagagtcc	atctgctgtg	aaggagagac	agagaactct	gggttccgtc	gtcctgtcca	180
cgtgctgtac	caagtgtctg	tgccagcctg	ttacctgttc	tctactgaaa	tctggctaata	240
gctcttgtgt	atcacttctg	attctgacaa	tcaatcaatc	aatggcctag	agcactgact	300
g						301

<210> 233
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 233						
atgactgact	tcccagtaag	gctctctaa	gggtaagtag	gaggatccac	aggatttgag	60
atgctaaggc	cccagagatc	gtttgatcca	accctcttat	tttcagaggg	gaaaatgggg	120
cctagaagt	acagagcatc	tagctgggtg	gctggcacc	ctggcctcac	acagactccc	180
gagtagctgg	gactacaggc	acacagtcac	tgaagcaggc	cctgttagca	attctatgcg	240
tacaaattaa	catgagatga	gtagagactt	tattgagaaa	gcaagagaaa	atcctatcaa	300
c						301

<210> 234
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 234						
aggtcctaca	catcgagact	catccatgat	tgatatgaat	ttaaaaatta	caagcaaaga	60
catttttattc	atcatgatgc	ttttttttgt	ttcttctttt	cgttttcttc	tttttttttt	120
tcaatttcag	caacatactt	ctcaatttct	tcaggattta	aaatcttgag	ggattgatct	180
cgctcatga	cagcaagttc	aatgtttttg	ccacctgact	gaaccacttc	caggagtgc	240
ttgatcacca	gttaaatggt	cagatcatct	gcttcaatgg	cttcgtcagt	atagttcttc	300
t						301

<210> 235
 <211> 283
 <212> DNA
 <213> Homo sapien

<400> 235
 tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg 60
 aattccctca tcttttaggg aatcatttac cagggttggg gaggattcag acagctcagg 120
 tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata 180
 atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatacaaca 240
 ttagggattc aaagaaatat tagatttaag ctcacactgg tca 283

<210> 236
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 236
 aggtcctcca ccaactgcct gaagcacggg taaaattggg aagaagtata gtgcagcata 60
 aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg 120
 tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatatag 180
 tgggtagacg gcttcatgag tacagtgtac tgtgggtatcg taatctggac ttgggttgta 240
 aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc 300
 a 301

<210> 237
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 237
 cagtggtagt ggtggtggac gtggcggttg tegtgggtgcc ttttttggtg cccgtcacaa 60
 actcaatttt tgttcgctcc tttttggcct tttccaattt gtccatctca attttctggg 120
 ccttggctaa tgctcatag taggagtcct cagaccagcc atggggatca aacatatacct 180
 ttgggtagtt ggtgccaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaatacta 240
 gggttccgaa attcttttct cctttggata atgtagttca tatccattcc ctcctttatc 300
 t 301

<210> 238
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 238
 gggcagggtt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt 60
 gttcacagtt cagccccctg ctcaaaaaac caacgggcca gctaaggaga ggaggaggca 120
 ccttgagact tccggagtcg aggctctcca gggttcccca gcccatcaat cattttctgc 180
 accccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca 240
 gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttcttta 300
 t 301

<210> 239
 <211> 239
 <212> DNA
 <213> Homo sapien

<400> 239
 ataagcagct aggggaattct ttatttagta atgtcctaac ataaaagttc acataactgc 60

ttctgtcaaa	ccatgatact	gagctttgtg	acaacccaga	aataactaag	agaaggcaaa	120
cataatacct	tagagatcaa	gaaacattta	cacagttcaa	ctgttttaaaa	atagctcaac	180
attcagccag	tgagtagagt	gtgaatgcc	gcatacacag	tatacaggtc	cttcaggga	239

<210> 240
 <211> 300
 <212> DNA
 <213> Homo sapien

<400> 240						
ggctcctaag	aagcagcagc	ttccacattt	taacgcagg	ttacgggtgat	actgtccttt	60
gggatctgcc	ctccagtgga	accttttaag	gaagaagtgg	gcccgaagcta	agttccacat	120
gctgggtgag	ccagatgact	tctgttcct	ggtcactttc	ttcaatgggg	cgaatggggg	180
ctgcagggtt	tttaaaatca	tgcttcatct	tgaagcacac	ggtcacttca	ccctcctcac	240
gctgtgggtg	tactttgatg	aaaataacca	ctttgttggc	ctttctgaag	ctataatgtc	300

<210> 241
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 241						
gaggtctggt	gctgaggtct	ctgggctagg	aagaggagtt	ctgtggagct	ggaagccaga	60
cctctttgga	ggaaactcca	gcagctatgt	tggtgtctct	gaggggaatgc	aacaaggctg	120
ctcctccatg	tattggaaaa	ctgcaaactg	gactcaactg	gaagggaagtg	ctgctgccag	180
tgtgaagaac	cagcctgagg	tgacagaaac	ggaagcaaac	aggaacagcc	agtcttttct	240
tcctctctct	gtcatacggg	ctctctcaag	catcctttgt	tgtcaggggc	ctaaaaggga	300
g						301

<210> 242
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 242						
ccgaggctct	gggatgcaac	caatcactct	gtttcacgtg	acttttatca	ccatacaatt	60
tgtggcattt	cctcattttc	tacattgtag	aatcaagagt	gtaaataaat	gtatatcgat	120
gtcttcaaga	atatatcatt	cctttttcac	tagaaccat	tcaaaatata	agtcaagaat	180
cttaatatca	acaaatatat	caagcaaact	ggaaggcaga	ataactacca	taatttagta	240
taagtaccca	aagttttata	aatcaaaagc	cctaagtata	accattttta	gaattcaatc	300
a						301

<210> 243
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 243						
aggtaagtcc	cagtttgaag	ctcaaaagat	ctgggtatgag	cataggctca	tcgacgacat	60
ggtggcccaa	gctatgaaat	cagagggagg	cttcatctgg	gcctgtaaaa	actatgatgg	120
tgacgtgcag	tcggactctg	tggcccaagg	gtatggctct	ctcggcatga	tgaccagcgt	180
gctggtttgt	ccagatggca	agacagtaga	agcagaggct	gcccacggga	ctgtaacccg	240
tcaactaccg	atgttccaga	aaggacagga	gacgtccacc	aatcccattg	cttccatttt	300
t						301

<210> 244
 <211> 300
 <212> DNA

83

<213> Homo sapien

<400> 244

gctggtttgc	aagaatgaaa	tgaatgattc	tacagctagg	acttaacctt	gaaatggaaa	60
gtcatgcaat	cccattttgca	ggatctgtct	gtgcacatgc	ctctgtagag	agcagcattc	120
ccagggacct	tggaacagct	tgacactgta	aggtgcttgc	tccccaagac	acatccctaaa	180
aggtgttgta	atggtgaaaa	cgtcttccct	ctttattgcc	ccttcttatt	tatgtgaaca	240
actgtttgtc	ttttgtgtat	cttttttaaa	ctgtaaagtt	caattgtgaa	aatgaatata	300

<210> 245

<211> 301

<212> DNA

<213> Homo sapien

<400> 245

gtctgagtat	ttaaaatggt	attgaaatta	tccccaacca	atgttagaaa	agaaagaggt	60
tatatactta	gataaaaaat	gaggtgaatt	actatccatt	gaaatcatgc	tcttagaatt	120
aaggccagga	gatattgtca	ttaatgtara	cttcaggaca	ctagagtata	gcagccctat	180
gttttcaaag	agcagagatg	caattaaata	ttgttttagca	tcaaaaaggc	cactcaatac	240
agctaataaa	atgaaagacc	taatttctaa	agcaattctt	tataatttac	aaagttttaa	300
g						301

<210> 246

<211> 301

<212> DNA

<213> Homo sapien

<400> 246

ggtctgtcct	acaatgcctg	cttcttgaaa	gaagtcggca	ctttctagaa	tagctaaata	60
acctgggctt	atttttaaaga	actattttgta	gctcagattg	gttttcctat	ggctaaaata	120
agtgcctctt	gtgaaaaatta	aataaaaacag	ttaattcaaa	gccttgatat	atgttaccac	180
taacaatcat	actaaatata	ttttgaagta	caaagtttga	catgctctaa	agtgacaacc	240
caaagtgtgc	ttacaaaaca	cgcttcctaac	aaggtatgct	ttacactacc	aatgcagaaa	300
c						301

<210> 247

<211> 301

<212> DNA

<213> Homo sapien

<400> 247

aggtcctttg	gcagggtctca	tggatcagag	ctcaaactgg	agggaaaggc	atttcgggta	60
gcctaagagg	gcgactggcg	gcagcacaaac	caaggaaggc	aaggttggtt	ccccacgct	120
gtgtcctgtg	ttcaggtgcg	acacacaatc	ctcatgggaa	caggatcacc	catgcgctgc	180
ccttgatgat	caaggttggg	gcttaagtgg	attaagggag	gcaagttctg	ggttccttgc	240
cttttcaaac	catgaagtca	ggctctgtat	ccctcctttt	cctaactgat	attctaacta	300
a						301

<210> 248

<211> 301

<212> DNA

<213> Homo sapien

<400> 248

aggtccttgg	agatgccatt	tcagccgaag	gactcttctw	ttcgggaagta	caccctcact	60
attaggaaga	ttcttagggg	taatttttct	gaggaaggag	aactagccaa	cttaagaatt	120
acaggaagaa	agtggtttgg	aagacagcca	aagaaataaa	agcagattaa	attgtatcag	180
gtacattcca	gcctgttggc	aactccataa	aaacatttca	gattttaatc	ccgaatttag	240

ctaagtacac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300
c 301

<210> 249
<211> 301
<212> DNA
<213> Homo sapien

<400> 249
gtccagagga agcacctggt gctgaactag gcttgccctg ctgtgaactt gcacttggag 60
ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgcgc 120
ccagggagac acagcagtga ctacagagctg gtcgcacact gtgcctccct cctcaccgcc 180
catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240
actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300
a 301

<210> 250
<211> 301
<212> DNA
<213> Homo sapien

<400> 250
ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc 60
cttatcttta ttggcttgat aaacataatt atttctaaca ctactgtatt tccagttgcc 120
cataagcaca tcagttacttt tctctggctg gaatagtaaa cttaaagtatg gtacatctac 180
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240
caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300
a 301

<210> 251
<211> 301
<212> DNA
<213> Homo sapien

<400> 251
gccgaggtcc tacatttggc ccagtttccc cctgcacact ctccagggcc cctgcctcat 60
agacaacctc atagagcata ggagaactgg ttgcccctggg ggcaggggga ctgtctggat 120
ggcagggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180
cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccggaa 240
cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct 300
c 301

<210> 252
<211> 301
<212> DNA
<213> Homo sapien

<400> 252
gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgttg catttccctca 60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata 120
tcattccttt ttactagga acccattcaa aatataagtc aagaatctta atatcaacaa 180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaagt 240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc 300
a 301

<210> 253
<211> 301
<212> DNA

<213> Homo sapien

<400> 253

ttccctaaga	agatgttatt	ttgttgggtt	ttgttcccc	tccatctoga	ttctcgtacc	60
caactaaaaa	aaaaaataa	agaaaaaatg	tgctgcgttc	tgaaaaataa	ctccttagct	120
tggtctgatt	gttttcagac	cttaaaaat	aaacttggtt	cacaagcttt	aatccatgtg	180
gatttttttt	cttagagaac	cacaaaacat	aaaaggagca	agtcggactg	aatacctgtt	240
tccatagtgc	ccacagggtg	ttcctcacat	tttctccata	ggaaaatgct	ttttcccaag	300
g						301

<210> 254

<211> 301

<212> DNA

<213> Homo sapien

<400> 254

cgctgcgcct	ttcccttggg	ggaggggcaa	ggccagaggg	ggtccaagtg	cagcacgagg	60
aacttgacca	attcccttga	agcgggtggg	ttaaaccctg	taaatgggaa	caaaatcccc	120
ccaaatctct	tcattcttacc	ctggtggact	cctgactgta	gaattttttg	gttgaaacaa	180
gaaaaaata	aagctttgga	cttttcaagg	ttgcttaaca	ggtactgaaa	gactggcctc	240
acttaaactg	agccaggaaa	agctgcagat	ttattaatgg	gtgtgttagt	gtgcagtggc	300
t						301

<210> 255

<211> 302

<212> DNA

<213> Homo sapien

<400> 255

agcttttttt	tttttttttt	tttttttttt	ttcattaaaa	aatagtgtct	tttattataa	60
attactgaaa	tgtttctttt	ctgaatataa	atataaatat	gtgcaaagtt	tgacttggat	120
tgggattttg	ttgagttctt	caagcatctc	ctaataccct	caagggcctg	agtagggggg	180
aggaaaaagg	actggaggtg	gaatctttat	aaaaaacaag	agtgattgag	gcagattgta	240
aacattatta	aaaaacaaga	aacaaacaaa	aaaatagaga	aaaaaaccac	cccaacacac	300
aa						302

<210> 256

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 256

gttccagaaa	acattgaagg	tggtttccca	aagtctaact	agggataccc	cctctagcct	60
aggaccctcc	tccccacacc	tcaatccacc	aaaccatcca	taatgcaccc	agataggccc	120
acccccaaaa	gcctggacac	cttgagcaca	cagttatgac	caggacagac	tcattcttat	180
aggcaaatag	ctgctggcaa	actggcatta	cctggtttgt	ggggatgggg	gggcaagtgt	240
gtggcctctc	ggcctgggta	gcaagaacat	tcagggttag	cctaagttan	tcgtgttagt	300
t						301

<210> 257

<211> 301

<212> DNA

<213> Homo sapien

<400> 257
 gttgtggagg aactctggct tgctcattaa gtcctactga ttttcactat cccctgaatt 60
 tccccactta tttttgtctt tcaactatcg aggccttaga agagggtctac ctgcctccag 120
 tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat 180
 gtcacattac tcccttcagt gatttcttgt agaagtgcc atccctgaat gccaccaaga 240
 tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300
 c 301

<210> 258
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 258
 cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60
 aggggcccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120
 cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg 180
 atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240
 tggatgatccc tgggagcgcc ggtggagtaa cgttgggtcca tggaaagcag cgcccacaac 300
 t 301

<210> 259
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 259
 tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg 60
 gtgtcctgaa gtgatttggg cccctgaggg cagacaccta agtaggaatc ccagtgggaa 120
 gcaaagccat aaggaagccc aggattcctt gtgatcagga agtggggccag gaaggctctgt 180
 tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt 240
 ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcaccccttg ctccagggtg 300
 c 301

<210> 260
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 260
 ttttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaaatt aagcaatggt 60
 aagggtgtctt aacttgaaaa agattaggag tcaactggttt acaagttata attgaatgaa 120
 agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaacia caggattaac 180
 tagggcaaaa taaataagtg tgtggaagcc ctgataagtg ctttaataaac agactgattc 240
 actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca 300
 c 301

<210> 261
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 261
 aaatattcga gcaaatcctg taactaatgt gtctccataa aaggctttga actcagtga 60
 tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt 120
 agcaccaact attccatata attcatcagc aggaaataaa ggctcttcag aaggttcaat 180
 ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag 240
 ggcgatgatga tcatccaaag cccagtgggc acttactcca gactttctgc aatgaagatc 300
 a 301

<210> 262
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 262
 gaggagagcc tgttacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc 60
 tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaattc ctgagtcacc 120
 cctagacttc ctaaaccaga tcctctgggg ctggaacctg gcaactctgca tttgtaatga 180
 gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtcccc 240
 catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat 300
 c 301

<210> 263
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (301)
 <223> n = A,T,C or G

<400> 263
 tttagcttgt ggtaaatgac tcacaaaact gatttttaaa tcaagttaat gtgaattttg 60
 aaaattacta cttaatccta attcacaata acaatggcat taagggttga cttgagttgg 120
 ttcttagtat tatttatggt aaataggctc ttaccacttg caaataactg gccacatcat 180
 taatgactga cttcccagta aggcctctta aggggtaagt angaggatcc acaggatttg 240
 agatgctaag gcccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg 300
 g 301

<210> 264
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 264
 aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaaacc 60
 aatgaatgac tctaaaaaca atattttacat ttaatggttt gtagacaata aaaaaacaag 120
 gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaag 180
 ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac 240
 acccttcata taaattcact atcttggtt gaggcactcc ataaaatgta tcacgtgcat 300
 a 301

<210> 265

<211> 301
 <212> DNA
 <213> Homo sapien

<400> 265
 tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcatctttgt 60
 cttcttgtga cgcagtatct cttctctggg gagaagccgg gaagtcttct cctggctcta 120
 catattcttg gaagtctcta atcaactttt gtccatttg tttcatttct tcaggaggga 180
 ttttcagttt gtcaacatgt tctctaacaa cacttgccca tttctgtaaa gaatccaaag 240
 cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg 300
 c 301

<210> 266
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 266
 taccgtctgc ccttctctcc atccaggcca tctgccaatc tacatgggtc ctcctattcg 60
 acaccagatc actccttccct ctaccacag gcttgctatg agcaagagac acaacctcct 120
 ctctctgttg ttccagcttc ttttctgttt cttcccaccc cttaagttct attcctgggg 180
 atagagacac caatacccat aacctctctc ctaagcctcc ttataacca ggggtgcacag 240
 cacagactcc tgacaactgg taaggccaat gaactgggag ctacacagctg gctgtgcctg 300
 a 301

<210> 267
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 267
 aaagagcaca ggccagctca gcctgccctg gccatctaga ctacagcctgg ctccatgggg 60
 gttctcagtg ctgagtcctat ccaggaaaag ctcaacctaga ccttctgagg ctgaatcttc 120
 atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtct ggagtaaagc 180
 ctcaattctga ttctctctct tcttttcttt caagttggct ttcctcacat ccctctgttc 240
 aattcgcttc agcttgtctg ctttagccct catttccaga agcttcttct ctttggcatc 300
 t 301

<210> 268
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 268
 aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta 60
 gatcttggga gagctgggtc ttctaaggag aaggagggaag gacagatgta actttggatc 120
 tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgttttagac tcttgggaata 180
 tgctgggtgg ctcaagtgag ccttttgagg aaagcaagta ttattcttaa ggagtaacca 240
 cttcccatg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact 300
 a 301

<210> 269
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 269
 taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60

```

aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact 120
atagtcacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta 180
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta 240
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300
t 301

```

```

<210> 270
<211> 301
<212> DNA
<213> Homo sapien

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<400> 270
cattgaagag cttttgcaa acatcagaac acaagtgcct ataaaattaa ttaagcctta 60
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120
gagcttgctg gtgcagtgc tattggataa cactattcat ggccgaattg atcaagtcaa 180
ccaactcctt gaactggatc atcagaagaa ggggtggtgca cgatatactg cactagataa 240
tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggcctt aacagaaac 300
a 301

```

```

<210> 271
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

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```

<400> 271
aaaaggttct cataagatta acaatttaaa taaatatttg atagaacatt ctttctcatt 60
tttatagctc atctttaggg ttgatattca gttcatgctt cccttgctgt tcttgatcca 120
gaattgcaat cacttcatca gcctgtatcc gotccaattc tctataaagt gggccaagg 180
tgaaccacag agccacagca cacctcttcc ccttggtgac tgccttcacc ccatganggt 240
tctctcctcc agatganaac tgatcatgcg cccacatttt gggttttata gaagcagtca 300
c 301

```

```

<210> 272
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 272
taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaatgtc 60
ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120
tccaataatt ccctcatgat gagcaagaaa aattctttgc gcacccctcc tgcattccaca 180
gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgttttc 240
ctaaggactt ccattgcata tcctacaata ttttctctac gcaccactag aattaagcag 300
g 301

```

```

<210> 273
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)

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<223> n = A,T,C or G

<400> 273

acatgtgtgt	atgtgtatct	ttgggaaaaan	aanaagacat	cttgtttayt	atTTTTTTTgg	60
agagangctg	ggacatggat	aatcacwtaa	tttgctayta	tyactTTaat	ctgactygaa	120
gaaccgtcta	aaaataaaaat	ttaccatgtc	dtatattcct	tatagtatgc	ttatttcacc	180
ttytttctgt	ccagagagag	tatcagtgc	ananatttma	gggtgaamac	atgmattggt	240
gggacttnty	tttacngagm	accctgcccg	sgcgcctcg	makngantt	ccgcsananc	300
t						301

<210> 274

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 274

cttatatact	ctttctcaga	ggcaaaagag	gagatgggta	atgtagacaa	ttctttgagg	60
aacagtaaat	gattattaga	gagaangaat	ggaccaagga	gacagaaatt	aacttgtaaa	120
tgattctctt	tggaatctga	atgagatcaa	gaggccagct	ttagcttggt	gaaaagtcca	180
tctaggatg	gttgcatctt	cgtcttcttt	tctgcagtag	ataatgaggt	aaccgaaggc	240
aattgtgctt	cttttgataa	gaagctttct	tggtcatatc	aggaaattcc	aganaaaagtc	300
c						301

<210> 275

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 275

tcggtgtcag	cagcacgtgg	cattgaacat	tgcaatgtgg	agcccaaacc	acagaaaatg	60
gggtgaaatt	ggccaacttt	ctattaactt	atgttggaac	ttttgccacc	aacagtaagc	120
tggtccctct	aataaaaagaa	aattgaaagg	tttctcacta	aacggaatta	agtagtgagg	180
tcaagagact	cccaggcctc	agcgtacctg	cccgggcggc	cgctcgaagc	cgaattctgc	240
agatatccat	cacactggcg	gncgctcgan	catgcatcta	gaaggnccaa	ttcgccctat	300
a						301

<210> 276

<211> 301

<212> DNA

<213> Homo sapien

<400> 276

tgtacacata	ctcaataaat	aatgactgc	attgtggtat	tattactata	ctgattatat	60
ttatcatgtg	acttctaatt	agaaaatgta	tccaaaagca	aaacagcaga	tatacaaaat	120
taaagagaca	gaagatagac	attaacagat	aaggcaactt	atacattgag	aatccaaatc	180
caatacattt	aaacattttg	gaaatgagg	ggacaaatgg	aagccagatc	aaatttgtgt	240
aaaactattc	agtatgtttc	ccttgcttca	tgtctgagaa	ggctctcctt	caatggggat	300
g						301

91

<210> 277
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 277
tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60
atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgcccc aacctgctct 180
caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga 240
gttcnctgtc gattacatct gaccagtctc cttttccga agtcnctcg ttcaatcttg 300
c 301

<210> 278
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 278
taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
cagtctctac tgttattatg cattacctgg gaatttataat aagcccttaa taataatgcc 180
aatgaacatc tcatgtgtgc tcacaatggt ctggcactat tataagtgtc tcacagggtt 240
tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
c 301

<210> 279
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 279
aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
gttatattaa ttgccaatat aagtaaataat agattatata tgtatagtgt ttcacaaagc 120
ttagaccttt accttccagc cccccacag tgcttgatat ttcagagtca gtcattgggt 180
atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
a 301

<210> 280
<211> 301
<212> DNA

<213> Homo sapien

<400> 280

ggtactggag	ttttcctccc	ctgtgaaaac	gtaactactg	ttgggagtga	attgaggatg	60
tagaaagggtg	gtggaaccaa	attgtgggtca	atggaaatag	gagaatatgg	ttctcactct	120
tgagaaaaaa	acctaagatt	agcccaggtg	gttgccctgta	acttcagttt	ttctgcctgg	180
gtttgatata	gttttagggtt	ggggtttagat	taagatctaa	attacatcag	gacaaagaga	240
cagactatta	actccacagt	taattaagga	ggtatgttcc	atgtttattt	gttaaagcag	300
t						301

<210> 281

<211> 301

<212> DNA

<213> Homo sapien

<400> 281

aggtacaaga	aggggaatgg	gaaagagctg	ctgctgtggc	attgttcaac	ttggatatctc	60
gccgagcaat	ccaaatcctg	aatgaagggg	catcttctga	aaaaggagat	ctgaatctca	120
atgtggtagc	aatggcttta	tcgggttata	cggatgagaa	gaactccctt	tgagagagaaa	180
tgtgtagcac	actgcgatta	cagctaaata	acccgtatct	gtgtgtcatg	tttgcatcttc	240
tgacaagtga	aacaggatct	tacgatggag	ttttgtatga	aaacaaagtt	gcagtacctc	300
g						301

<210> 282

<211> 301

<212> DNA

<213> Homo sapien

<400> 282

caggtactac	agaattaaaa	tactgacaag	caagtagttt	cttggcgtgc	acgaattgca	60
tccagaaccc	aaaaattaag	aaattcaaaa	agacattttg	tgggcacctg	ctagcacaga	120
agcgcagaag	caaagcccag	gcagaacat	gctaaccctt	cagctcagcc	tgacagagaag	180
cgcaagaagca	aagcccaggc	agaaccatgc	taaccttaca	gctcagcctg	cacagaagcg	240
cagaagcaaa	gccccaggcag	aacatgctaa	ccttacagct	cagcctgcac	agaagcacag	300
a						301

<210> 283

<211> 301

<212> DNA

<213> Homo sapien

<400> 283

atctgtatac	ggcagacaaa	ctttatarag	tgtagagagg	tgagcgaaaag	gatgcaaaaag	60
cactttgagg	gctttataat	aatatgctgc	ttgaaaaaaa	aaatgtgtag	ttgatactca	120
gtgcatctcc	agacatagta	aggggttgct	ctgaccaatc	aggtgatcat	tttttctatc	180
acttcccagg	ttttatgcaa	aaattttgtt	aaattctata	atgggtgatat	gcatctttta	240
ggaaacatat	acatttttaa	aaatctatct	tatgtaagaa	ctgacagacg	aatttgcttt	300
g						301

<210> 284

<211> 301

<212> DNA

<213> Homo sapien

<400> 284

caggtacaaa	acgctattaa	gtggcttaga	atttgaacat	ttgtggtctt	tatttacttt	60
gcttcgtgtg	tgggcagaagc	aacatcttcc	ctaaatatat	attaccaaga	aaagcaagaa	120
gcagattagg	tttttgacaa	aacaaacagg	ccaaaagggg	gctgacctgg	agcagagcat	180

93

ggtgagaggc aaggcatgag agggcaagtt tgttgtggac agatctgtgc ctactttatt 240
 actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300
 a 301

<210> 285
 <211> 301
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 285
 acatcaccat gatcggatcc cccacccatt atacgttgta tgtttacata aatactcttc 60
 aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120
 caggaaagca aatgctatct acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
 attaaatatg tctgacttct tttgaggcca cagcactagg caaatgctat ttacgatctg 240
 caaagctgtg ttgaagagtc aaagcccca tgtgaacacg atttctggac cctgtaacag 300
 t 301

<210> 286
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 286
 taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60
 tgtatattat ttttgcctta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
 atcaaaatgt gtcattgccag taagagatgt tatattcttt tctcatttct tccccacca 180
 aaaataagct accatatagc ttataagtct caaatttttg ctttttacta aaatgtgatt 240
 gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt tttcccttg 300
 t 301

<210> 287
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 287
 tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
 cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg 120
 aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc 180
 cagtgttat ctctcccca gcttggctgc ctcatgttat cacagtattc cttttgttt 240
 gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc 300
 t 301

<210> 288
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 288
 gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
 agtcaatagg aagacaaatt ccagttccag ctcatgtctg gtatctgcaa agctgcaaaa 120
 gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180
 aaaagcatct gcttttgtga ttttaatttag ctcatctggc cactggaaga atccaaacag 240

tctgccttaa ttttggatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
a 301

<210> 289
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 289
ggtacactgt ttccatgtta tgttttotaca cattgctacc tcagtgtctc tggaaactta 60
gcttttggatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg 120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa 180
cgttctataa atgaatgtgc tgaagcaaa tgcccatggt ggcggcgaan aagagaaaga 240
tgtgttttgt tttggactct ctgtgggtccc ttccaatgct gtgggtttcc aaccagnnga 300
a 301

<210> 290
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 290
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac 60
tgactgatct gttcatttct ctcacagctc ttaccccaaa aagcttttcc accctaagtg 120
ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg 180
gagttctatc aagaggcgaga aacagcacag aatcccagtt ttaccattcg ctgacagtgc 240
tgccttgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagttag 300
a 301

<210> 291
<211> 301
<212> DNA
<213> Homo sapien

<400> 291
caggtagcaa tttcttctat cctagaaaca tttcatttta tgttgttgaa acataacaac 60
tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc 120
tttactcttt tgtttatagg tgaatcacia aatgtatttt tatgtattct gtagttcaat 180
agccatggct gtttacttca ttttaatttat ttagcataaa gacattatga aaaggcctaa 240
acatgagctt cacttcccca ctaactaatt agcatctggt atttcttaac cgtaatgcct 300
a 301

<210> 292
<211> 301
<212> DNA
<213> Homo sapien

<220>

95

<221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 292
 accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc 60
 tgtattaaat aattttttaag tttaaaagat aaaataccat catttttaa atgttggtattc 120
 aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaaatgat ttgcnagatg 180
 ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc 240
 tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa 300
 a 301

<210> 293
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 293
 ggtaccaagt gctggtgcca gcctgttacc tgttctcact gaaaagtctg gctaattgctc 60
 ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcctagagc actgactgtt 120
 aacacaaacg ttagtagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt 180
 gtgagaatth tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg 240
 ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300
 g 301

<210> 294
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 294
 tgacccataa caatatacac tagctatctt ttttaactgtc catcattagc accaatgaag 60
 attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag 120
 ttttaactata gtcacaganc ttaaataatc acattgtttt ctatgtctac tgaaaataag 180
 ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240
 cccaattata cagtagcaca accaccttat gtagttttta catgtagact ctgtagaggt 300
 t 301

<210> 295
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 295
 gtactctttc tctccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60
 cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120
 ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccactctctga 180
 actggtagaa aaacrtctga agagctagtc tatcagcatc tgacaggtga attggatggg 240
 tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300
 tctct 305

<210> 296
 <211> 301

96

<212> DNA

<213> Homo sapien

<400> 296

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aggtagctatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct      60
cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg      120
attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac      180
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt      240
tgtcattact ataaatttta aaatctgtta ataagatggc ctataggagg gaaaaagggg      300
c

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<210> 297

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 297

```

actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta      60
aaggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga      120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt      180
tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtgggc      240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aactggcgg      300

```

<210> 298

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 298

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tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccggg      60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg      120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccacct      180
gtcctgtctg ttacatttc actaycaggt tttctctggg cattacnatt tgttccccta      240
caacagtgc ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg      300
t

```

<210> 299

<211> 301

<212> DNA

<213> Homo sapien

<400> 299

```

gttttgagac ggagtttcac tcttggtgcc cagactggac tgcaatggca ggggtctctgc      60
tcaactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc      120
tggtgattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg      180
gagtttgcgc atgttgacca gctgggtctca aactcctgac ctcaagcgac ctgcctgcct      240
cggcctccca aagtgcctga attataggca tgagtcaaca cgcccagcct aaagatatatt      300
t

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97

<210> 300
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 300
 attcagtttt atttgcgtgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60
 tatgtccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca 120
 gctgcattcc acaaggttct cagcctaata agtttacta cctgccagtc tcaaaactta 180
 gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttggtac 240
 tataaagcct gcctctaaca gtcccttgctt cttcacacca atcccagagc catcccccat 300
 g 301

<210> 301
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 301
 tttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60
 agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggg 120
 gggaactcac aaagaccctc agagctgaga caccacaaac agtgggagct cacaaagacc 180
 ctcagagctg agacaccac aacagtggga gctcacaaag accctcagag ctgagacacc 240
 cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300
 t 301

<210> 302
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 302
 aggtacacat ttagcttggt gtaaataact cacaaaactg attttaaaat caagttaatg 60
 tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac 120
 ttgagttggg tcttagtatt atttatggta aataggctct taccacttgc aaataactgg 180
 ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca 240
 caggatttga gatgctaagg ccccagagat cgtttgatcc aaccctctta ttttcagagg 300
 g 301

<210> 303
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 303
 aggtaccaac tgtggaaata ggtagaggat ctttttttct ttccatatca actaagttgt 60
 atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcao 120
 tggctaattg aactaccgct tgcattgtaa aaatgggtgt ttgtgaaatg atcataggcc 180
 agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc 240
 catcgatttt atatctgggg tctagaaaaa gagttaatct gttttccctc ataaattcac 300
 c 301

<210> 304
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 304
 acatggatgt tatatttcag actgtcaacc tgaatttgta tttgcttgac attgcctaata 60
 tattagtttc agtttcagct taccactttt ttgtctgcaa catgcaraas agacagtgcc 120
 ctttttagtg tatcatatca ggaatcatct cacattgggt tgtgccatta ctgggtgcagt 180
 gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga 240
 ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct 300
 c 301

<210> 305
 <211> 301
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 305
 gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag 60
 cagggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggag 120
 taaaggagga gaaacagata caaatctcc aactcagtat taaggatttc tcatgcctag 180
 aatattggta gaaacaagaa tacattcata tggcaaataa ctaaccatgg tggacaacaaa 240
 ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag 300
 a 301

<210> 306
 <211> 8
 <212> PRT
 <213> Homo sapien

<400> 306
 Val Leu Gly Trp Val Ala Glu Leu
 1 5

<210> 307
 <211> 637
 <212> DNA
 <213> Homo sapien

<400> 307
 acagggtratg aagggaaagg gagaggatga ggaagcccc ctggggattt ggtttgggtcc 60
 ttgtgatcag gtggtctatg gggttatcc ctacaaagaa gaatccagaa ataggggcac 120
 attgaggaat gatacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt 180
 cacaccattg gtgagggagg gattaccacc ctgggggttat gaagatggtt gaacacccca 240
 cacatagcac cggagatatg agatcaacag ttcttagcc atagagattc acagcccaga 300
 gcaggaggac gcttgccacac catgcaggat gacatggggg atgcgctcgg gattggtgtg 360
 aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacgggtggg caaactctga 420
 tttccgtggg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagtga 480
 actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca 540
 ggtgggagcc ttcccgatg ggtgtgggac atatctggca agattttgtg gcactcctgg 600
 ttacagatac tggggcagca aataaaactg aatcttg 637

<210> 308
 <211> 647
 <212> DNA
 <213> Homo sapien

99

<220>
 <221> misc_feature
 <222> (1)...(647)
 <223> n = A,T,C or G

<400> 308
 acgattttca ttatcatgta aatcgggtca ctcaaggggc caaccacagc tgggagccac 60
 tgctcagggg aaggttcata tgggactttc tactgcccaa gggtctatac aggatataaa 120
 ggngcctcac agtatagatc tggtagcaaa gaagaagaaa caaacactga tctctttctg 180
 ccacccctct gaccctttgg aactcctctg acccttttaga acaagcctac ctaatatctg 240
 ctagagaaaa gaccaacaac ggcctcaaaag gatctcttac catgaaggtc tcagctaatt 300
 cttggctaag atgtgggttc cacattaggt tctgaatatg gggggaagg tcaatttgct 360
 cattttgtgt gtggataaag tcaggatgcc caggggccag agcagggggc tgcttgcttt 420
 gggaacaatg gctgagcata taaccatagg ttatggggaa caaaacaaca tcaaagtcac 480
 tgtatcaatt gccatgaaga cttgagggac ctgaatctac cgattcatct taaggcagca 540
 ggaccagttt gagtggcaac aatgcagcag cagaatcaat ggaaacaaca gaatgattgc 600
 aatgtccttt tttttctcct gcttctgact tgataaaagg ggaccgt 647

<210> 309
 <211> 460
 <212> DNA
 <213> Homo sapien

<400> 309
 actttatagt ttaggctgga cattggaaaa aaaaaaaagc cagaacaaca tgtgatagat 60
 aatatgattg gctgcacact tccagactga tgaatgatga acgtgatgga ctattgtatg 120
 gagcacatct tcagcaagag ggggaaatac tcatcathtt tggccagcag ttgtttgatc 180
 accaaacatc atgccagaat actcagcaaa ccttcttagc tcttgagaag tcaaagtccg 240
 ggggaattta ttcctggcaa ttttaattgg actccttatg tgagagcagc ggctaccag 300
 ctggggtggt ggagcgaacc cgtcactagt ggacatgcag tggcagagct cctggtaacc 360
 acctagagga atacacaggc acatgtgtga tgccaagcgt gacacctgta gcactcaaat 420
 ttgtcttgtt tttgtctttc ggtgtgtaag attcttaagt 460

<210> 310
 <211> 539
 <212> DNA
 <213> Homo sapien

<400> 310
 acgggactta tcaaataaag ataggaaaag aagaaaactc aaatattata ggcagaaatg 60
 ctaaagggtt taaaatatgt caggattgga agaaggcatg gataaagaac aaagttcagt 120
 taggaaagag aaacacagaa ggaagagaca caataaaagt cattatgtat tctgtgagaa 180
 gtcagacagt aagattttgtg ggaaatgggt tggtttgttg tatggtatgt attttagcaa 240
 taatctttat ggcagagaaa gctaaaatcc tttagcttgc gtgaatgatc acttgctgaa 300
 ttcctcaagg taggcatgat gaaggagggt ttagaggaga cacagacaca atgaactgac 360
 ctagatagaa agccttagta tactcagcta ggaatagtga ttctgagggc aactgtgac 420
 atgattatgt cattacatgt atggtagtga tggggatgat aggaaggaag aacttatggc 480
 atattttcac ccccaaaaa gtcagttaaa tattgggaca ctaaccatcc aggtcaaga 539

<210> 311
 <211> 526
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(526)
 <223> n = A,T,C or G

100

<400> 311

caaatttgag	ccaatgacat	agaattttac	aaatcaagaa	gcttattctg	gggccatttc	60
ttttgacgtt	ttctctaaac	tactaaagag	gcattaatga	tccataaatt	atattatcta	120
catttacagc	atttaaaatg	tgttcagcat	gaaatattag	ctacagggga	agctaaataa	180
attaaacatg	gaataaagat	ttgtccttaa	atataatcta	caagaagact	ttgatatttg	240
tttttcacaa	gtgaagcatt	cttataaaagt	gtcataacct	ttttggggaa	actatgggaa	300
aaaatgggga	aactctgaag	ggttttaagt	atcttacctg	aagctacaga	ctccataacc	360
tctctttaca	gggagctcct	gcagccccta	cagaaatgag	tggctgagat	tcttgattgc	420
acagcaagag	cttctcatct	aaaccctttc	cctttttagt	atctgtgtat	caagtataaa	480
agttctataa	actgtagtnt	acttattttta	atccccaaag	cacagt		526

<210> 312

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 312

cctctctctc	cccaccccct	gactctagag	aactgggttt	tctcccagta	ctccagcaat	60
tcattttctga	aagcagttga	gccactttat	tccaaagtac	actgcagatg	ttcaaactct	120
ccattttctct	ttcccttcca	cctgccagtt	ttgctgactc	tcaacttgct	atgagtgtaa	180
gcattaagga	cattatgctt	cttcgattct	gaagacaggc	cctgctcatg	gatgactctg	240
gcttcttagg	aaaatatatt	tcttccaaaa	tcagtaggaa	atctaaactt	atcccctctt	300
tgcagatgtc	tagcagcttc	agacatttgg	ttaagaacct	atgggaaaaa	aaaaaatcct	360
tgctaattgt	gtttcctttg	ttaaccanga	ttcttatttg	nctggtatag	aatatcagct	420
ctgaacgtgt	ggtaaagatt	tttgtgtttg	aatataggag	aatcagttt	gctgaaaagt	480
tagtcttaat	tatctattgg					500

<210> 313

<211> 718

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(718)

<223> n = A,T,C or G

<400> 313

ggagatttgt	gtggtttgca	gccgaggag	accaggaaga	tctgcatggt	gggaaggacc	60
tgatgataca	gaggtgagaa	ataagaaagg	ctgctgactt	taccatctga	ggccacacat	120
ctgctgaaat	ggagataatt	aacatcacta	gaaacagcaa	gatgacaata	taatgtctaa	180
gtagtgacat	gtttttgcac	atttccagcc	cttttaaata	tccacacaca	caggaagcac	240
aaaaggaaagc	acagagatcc	ctgggagaaa	tgcccggccg	ccatcttggg	tcacgatga	300
gcctcgccct	gtgcctgntc	ccgcttgtag	gggaaggaca	ttagaaaatg	aattgatgtg	360
ttccttaaaag	gatggcagga	aaacagatcc	tgttgtggat	atttatttga	acgggattac	420
agatttgaaa	tgaagtcaca	aagtgagcat	taccaatgag	aggaaaacag	acgagaaaat	480
cttgatgggt	cacaagacat	gcaacaaaca	aaatggaata	ctgtgatgac	acgagcagcc	540
aactggggag	gagataccac	ggggcagagg	tcaggattct	ggccctgctg	cctaactgtg	600
cgttatacca	atcatttcta	tttctaccct	caaacaagct	gtngaatatc	tgacttacgg	660
ttcttntggc	ccacattttc	atnatccacc	ccntcntttt	aannttantc	caantgt	718

<210> 314

101

<211> 358
 <212> DNA
 <213> Homo sapien

<400> 314
 gtttattttac attacagaaa aaacatcaag acaatgtata ctatttcaaa tatatccata 60
 cataatcaaa tatagctgta gtacatgttt toattgggtg agattaccac aaatgcaagg 120
 caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa 180
 gctctcggta gtccagccac tgtgaaacat gctcccttta gattaacctc gtggacgctc 240
 ttgtttgtatt gctgaactgt agtgccctgt attttgcttc tgtctgtgaa ttctgttgct 300
 tctggggcat ttcttgtga tgcagaggac caccacacag atgacagcaa tctgaatt 358

<210> 315
 <211> 341
 <212> DNA
 <213> Homo sapien

<400> 315
 taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc 60
 ataggtgatg atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt 120
 gacccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag ccccaatgac 180
 agtcaccagc tccccgacca gccggatata gtccttaggg gtcagttagg ctctctgaag 240
 tagcttctgc tgtaagaggg tggtgtcccg ggggctcgtg cggttattgg tcctgggctt 300
 gagggggcgg tagatgcagc acatggtgaa gcagatgatg t 341

<210> 316
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 316
 agactgggca agactcttac gccccacact gcaatttggt cttgttgccg tatccattta 60
 tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact 120
 cattcaggga gctctggttg caatattagt t 151

<210> 317
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 317
 agaactagtg gatcctaattg aaataacctga aacatatatt ggcatttatc aatggctcaa 60
 atcttcattt atctctggcc ttaaccctgg ctccctgaggc tgcggccagc agatcccagg 120
 ccagggtctt gttcttgcca cacctgcttg a 151

<210> 318
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 318
 actggtggga ggcgctgttt agttggctgt ttccagaggg gtctttcgga gggacctcct 60
 gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg 120
 tgggggcggg ttatcaggca gtgataaaca t 151

<210> 319
 <211> 151
 <212> DNA

102

<213> Homo sapien

<400> 319

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aactagtgga tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta      60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg      120
taagattggg tttatgtgat tttagtgggt a                                     151

```

<210> 320

<211> 150

<212> DNA

<213> Homo sapien

<400> 320

```

aactagtgga tccactagtc cagtgtggtg gaattccatt gtgttggggg tctagatcgc      60
gagcggctgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt      120
gagtgttcta cagcttacag taaataccat                                     150

```

<210> 321

<211> 151

<212> DNA

<213> Homo sapien

<400> 321

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agcaactttg tttttcatcc aggttatattt aggccttagga tttcctctca cactgcagtt      60
taggggtggc ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg      120
tgcctctgag aaatcaaagt cttcatacac t                                     151

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<210> 322

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 322

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atccagcatc ttctcctggt tcttgccttc ctttttcttc ttcttasatt ctgcttgagg      60
tttgggcttg gtcagtttgc cacagggtt ggagatggtg acagtcttct ggcattcggc      120
attgtgaggg gctcgttca naattccagt t                                     151

```

<210> 323

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

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tgaggacttg tktttctttt ctttattttt aatcctctta ckttgtaaata atattgccta      60
nagactcant tactaccag tttgtgggtt twtgggagaa atgtaactgg acagttagct      120
gttcaatyaa aaagacactt ancccatgtg g                                     151

```

<210> 324

103

<211> 461
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(461)
 <223> n = A,T,C or G

<400> 324

acctgtgtgg	aatttcagct	ttcctcatgc	aaaaggattt	tgtatccccg	gcctacttga	60
agaagtggtc	agctaaagga	atccagggtg	ttgggtggac	tgtaataacc	tttcatgaaa	120
agagttacta	cgaatcccat	cttggttcca	gctatatcac	tgacagcatg	gtagaagact	180
gcgaacctca	cttctagact	ttcacggtgg	gacgaaacgg	gttcagaaac	tgccaggggc	240
ctcatacagg	gatatacaaa	taccctttgt	gctacccagg	ccctggggaa	tcaggtgact	300
cacacaaatg	caatagttgg	tactgcatt	tttacctgaa	ccaaagctaa	acccggtggt	360
gccacatg	accatggcat	gccagagttc	aacactgttg	ctcttgaaaa	ttgggtctga	420
aaaaacgcac	aagagcccct	gccctgcct	agctgangca	c		461

<210> 325
 <211> 400
 <212> DNA
 <213> Homo sapien

<400> 325

acactgtttc	catgttatgt	ttctacacat	tgctacctca	gtgctcctgg	aaacttagct	60
tttcatgtct	ccaagtagtc	caccttcatt	taactctttg	aaactgtatc	atctttgccca	120
agtaagagtg	gtggcctatt	tcagctgctt	tgacaaaatg	actggctcct	gacttaacgt	180
tctataaatg	aatgtgctga	agcaaagtgc	ccatggtggc	ggcgaagaag	agaaagatgt	240
gttttgtttt	ggactctctg	tggtcccttc	caatgctgtg	ggtttccaac	caggggaagg	300
gtcccttttg	cattgccaag	tgccataacc	atgagcacta	cgctaccatg	gttctgcctc	360
ctggccaagc	aggctgggtt	gcaagaatga	aatgaatgat			400

<210> 326
 <211> 1215
 <212> DNA
 <213> Homo sapien

<400> 326

ggaggactgc	agcccgcaact	cgcagccctg	gcaggcgcca	ctgggtcatgg	aaaacgaatt	60
gttctgtctg	ggcgtcctgg	tgcatccgca	gtgggtgctg	tcagccgcac	actgtttcca	120
gaactcctac	accatcgggc	tgggcctgca	cagtcttgag	gccgaccaag	agccagggag	180
ccagatgggtg	gaggccagcc	tctccgtacg	gcacccagag	tacaacagac	ccttgctcgc	240
taacgacctc	atgctcatca	agttggacga	atccgtgtcc	gagtctgaca	ccatccggag	300
catcagcatt	gcttcgcagt	gccctaccgc	ggggaactct	tgccctcgttt	ctggctgggg	360
tctgctggcg	aacggcagaa	tgccctaccgt	gctgcagtgc	gtgaacgtgt	cgggtggtgc	420
tgaggaggtc	tgcatgaagc	tctatgaccc	gctgtaccac	cccagcatgt	tctgcgccgg	480
cggagggcaa	gaccagaagg	actcctgcaa	cggtgactct	ggggggcccc	tgatctgcaa	540
cgggtacttg	cagggccttg	tgtctttcgg	aaaagccccg	tgtggccaag	ttggcgtgcc	600
aggtgtctac	accaacctct	gcaaattcac	tgagtggata	gagaaaaccg	tccaggccag	660
ttaaactctg	ggactgggaa	cccatgaaat	tgacccccaa	atacatcctg	cgggaaggaat	720
tcaggaatat	ctgttcccag	cccctcctcc	ctcaggccca	ggagtccagg	ccccagcccc	780
ctcctccctc	aaaccaaggg	tacagatccc	cagccccctc	tccctcagac	ccaggagtcc	840
agacccccca	gccccctcct	cctcagaccc	aggagtccag	ccccctcctc	ctcagaccca	900
ggagtccaga	ccccccagcc	cctcctccct	cagacccagg	ggtccaggcc	cccaaccctt	960
cctccctcag	actcagaggt	ccaagcccc	aacccctcct	tccccagacc	cagaggtcca	1020
ggtcccagcc	cctcctccct	cagacccagc	ggtccaatgc	cacctagact	ctccctgtac	1080
acagtgcccc	cttgtggcac	gttgacccaa	ccttaccagt	tggtttttca	ttttttgtcc	1140

104

ctttcccta gatccagaaa taaagtctaa gagaagcgca aaaaaaaaaa aaaaaaaaaa 1200
 aaaaaaaaaa aaaaaa 1215

<210> 327
 <211> 220
 <212> PRT
 <213> Homo sapien

<400> 327

Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Val	Met
1				5					10					15	
Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val
			20					25					30		
Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu	Gly
	35						40					45			
Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val	Glu
	50					55					60				
Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu	Ala
65					70					75					80
Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser	Asp
			85						90					95	
Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly	Asn
			100					105					110		
Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met	Pro
		115					120					125			
Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Glu	Val	Cys
	130					135					140				
Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly
145					150					155					160
Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly	Pro
			165						170					175	
Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys	Ala
			180					185					190		
Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys
		195					200					205			
Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser				
	210					215					220				

<210> 328
 <211> 234
 <212> DNA
 <213> Homo sapien

<400> 328

cgctcgtctc	tggtagctgc	agccaaatca	taaacggcga	ggactgcagc	ccgcactcgc	60
agccctggca	ggcggcactg	gtcatggaaa	acgaattgtt	ctgctcgggc	gtcctgggtgc	120
atccgcagtg	ggtgctgtca	gccacacact	gtttccagaa	ctcctacacc	atcgggctgg	180
gcctgcacag	tcttgaggcc	gaccaagagc	cagggagcca	gatggtggag	gccca	234

<210> 329
 <211> 77
 <212> PRT
 <213> Homo sapien

<400> 329

Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile	Asn	Gly	Glu	Asp	Cys	Ser
1				5					10					15	
Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Val	Met	Glu	Asn	Glu	Leu

105

	20		25		30
Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr					
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<212> DNA

<213> Homo sapien

<400> 334

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<400> 336
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 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 50 55 60
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
 65 70 75 80
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
 85 90 95
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
 100 105 110
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
 115 120 125
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
 130 135 140
 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
 145 150 155 160
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
 165 170 175
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
 180 185 190
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
 195 200 205
 Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
 210 215 220
 Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
 225 230 235 240
 Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
 245 250 255
 Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
 260 265 270
 Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
 275 280 285
 Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
 290 295 300
 Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
 305 310 315

<210> 340

<211> 483

<212> DNA

<213> Homo sapien

<400> 340

gccgagggtct gccttcacac ggaggacacg agactgcttc ctcaagggct cctgcctgcc 60
 tggacactgg tgggaggcgc tggttagttg gctgttttca gaggggtctt tcggagggac 120
 ctctgctgc aggttgaggt gtctttattc ctggcgggag accgcacatt ccactgctga 180
 gggtgtgggg gcggtttatc aggcagtgat aaacataaga tgtcatttcc ttgactccgg 240
 ccttcaattt tctctttggc tgacgacgga gtccgtggtg tcccgatgta actgaccct 300
 gctccaaacg tgacatcact gatgctcttc tcgggggtgc tgatggcccg cttggtcacg 360
 tgctcaatct cgccattcga ctcttgctcc aaactgtatg aagacacctg actgcacgtt 420
 ttttctgggc ttccagaatt taaagtgaag ggcagcactc ctaagctccg actccgatgc 480
 ctg 483

111

<210> 341
 <211> 344
 <212> DNA
 <213> Homo sapien

<400> 341
 ctgctgctga gtcacagatt tcattataaa tagcctccct aaggaaaata cactgaatgc 60
 tttttttact aaccatttcta tttttataga aatagctgag agtttctaaa ccaactctct 120
 gctgccttac aagtattaaa ttttttactt ctttccataa agagtagctc aaaatatgca 180
 attaatttaa taatttctga tgatgggttt atctgcagta atatgtatat catctattag 240
 aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300
 ctgattctta acattgtctt taatgaccac aagacaacca acag 344

<210> 342
 <211> 592
 <212> DNA
 <213> Homo sapien

<400> 342
 acagcaaaaa agaaactgag aagcccaaty tgctttcttg ttaacatcca cttatccaac 60
 caatgtggaa acttcttata cttggttcca ttatgaagtt ggacaattgc tgctatcaca 120
 cctggcaggt aaaccaatgc caagagagtg atggaaacca ttggcaagac tttgttgatg 180
 accaggattg gaattttata aaaatattgt tgatgggaag ttgctaaagg gtgaattact 240
 tccctcagaa gagtgtaaag aaaagtcaga gatgctataa tagcagctat ttttaattggc 300
 aagtgccact gtggaaagag ttcctgtgtg tgctgaagtt ctgaagggca gtcaaattca 360
 tcagcatggg ctgtttggtg caaatgcaaa agcacaggtc tttttagcat gctggctctc 420
 cccgtgtcct tatgcaaata ategtcttct tctaaatttc tcctaggctt cattttccaa 480
 agttcttctt ggtttgtgat gtcttttctg ctttccatta attctataaa atagtatggc 540
 ttcagccacc cactcttcgc cttagcttga ccgtgagtc cggctgccgc tg 592

<210> 343
 <211> 382
 <212> DNA
 <213> Homo sapien

<400> 343
 ttcttgacct cctcctcctt caagctcaaa caccacctcc cttattcagg accggcactt 60
 cttaatgttt gtggctttct ctccagcctc tcttaggagg ggtaatggtg gaggttggcat 120
 cttgtaactc tcctttctcc tttcttcccc tttctctgcc cgcttttccc atcctgctgt 180
 agacttcttg attgtcagtc tgtgtcacat ccagtgattg ttttggttcc tgttcccttt 240
 ctgactgccc aaggggctca gaaccccagc aatcccttcc tttcactacc ttcttttttg 300
 ggggtagttg gaagggactg aaattgtggg gggaaggtag gaggcacatc aataaagagg 360
 aaaccaccaa gctgaaaaaa aa 382

<210> 344
 <211> 536
 <212> DNA
 <213> Homo sapien

<400> 344
 ctgggcctga agctgtaggg taaatcagag gcaggcttct gagtgatgag agtcctgaga 60
 caataggcca cataaacttg gctggatgga aacctacaat aagggtgtca cctcttggtt 120
 gtttaggggg atgccaagga taaggccagc tcagttatat gaagagaagc agaacaaaca 180
 agtctttcag agaaatggat gcaatcagag tgggatcccg gtcacatcaa ggtcacactc 240
 caccttcatg tgctgaaatg gttgccaggc cagaaaaatc cacccttac gagtgcggct 300
 tcgacccat atccccgcc cgggtccctt tctccataaa attcttctta gtagctatta 360
 ccttcttatt atttgatcta gaaattgcc tctttttacc cctaccatga gccctacaaa 420

112

caactaacct gccactaata gttatgtcat cctctttatt aatcatcatc ctagccctaa 480
gtctggccta tgagtgacta caaaaaggat tagactgagc cgaataacaa aaaaaa 536

<210> 345
<211> 251
<212> DNA
<213> Homo sapien

<400> 345
accttttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg 60
tgaatgaagc ccccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggactttg 120
gctgtgggcca ggaaatcaca tcctacactg cccaggagcc agacacattt atggaacaga 180
aaataacata tcggatttgg agagacactg ccaactggct ggagattaat ccggacactg 240
gtgccatttc c 251

<210> 346
<211> 282
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(282)
<223> n = A,T,C or G

<400> 346
cgctgtctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt 60
ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcagttaca aattctggga 120
agggagacta tacctggctc ttgccctaag tgagaggtct tccctcccg cccaaaaaat 180
agaaaggctt tctatttcac tggcccagggt agggggaagg agagtaactt tgagtctgtg 240
ggtctcattt cccaaggtgc cttcaatgct catnaaaacc aa 282

<210> 347
<211> 201
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(201)
<223> n = A,T,C or G

<400> 347
acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca 60
taaataatac ttttaaaaana ntactancag cttttaccta ngctcctaaa tgcttgtaaa 120
tgtgagactg actggaccca cccagaccca gggcaaagat acatgttacc atatcatctt 180
tataaagaat ttttttttgt c 201

<210> 348
<211> 251
<212> DNA
<213> Homo sapien

<400> 348
ctgttaatca caacatttgt gcatcacttg tgccaagtga gaaaatgttc taaaatcaca 60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga 120
aggagacact ccagcatgg aggagggtt atcttttcat cctaggtcag gtctacaatg 180
ggggaagggtt ttattataga actcccaaca gccacactca ctccctgccac ccacccgatg 240

113

gccctgcctc c

251

<210> 349

<211> 251

<212> DNA

<213> Homo sapien

<400> 349

taaaaatcaa	gccatttaaat	tgtatctttg	aaggtaaaca	atatatggga	gctggatcac	60
aaccctgag	gatgccagag	ctatgggtcc	agaacatggg	gtggtattat	caacagagtt	120
cagaagggtc	tgaactctac	gtgttaccag	agaacataat	gcaattcatg	cattccactt	180
agcaattttg	taaaatacca	gaaacagacc	ccaagagtct	ttcaagatga	ggaaaattca	240
actcctggtt	t					251

<210> 350

<211> 908

<212> DNA

<213> Homo sapien

<400> 350

ctggacactt	tgcgagggct	tttgcctggc	gtgctgctg	cccgtcatgc	tactcatcgt	60
agcccgcccg	gtgaagctcg	ctgctttccc	tacctcctta	agtgactgcc	aaacgcccac	120
cggctggaat	tgctctgggt	atgatgacag	agaaaatgat	ctcttcctct	gtgacaccaa	180
cacctgtaaa	tttgatgggg	aatgtttaag	aattggagac	actgtgactt	gcgtctgtca	240
gttcaagtgc	aacaatgact	atgtgcctgt	gtgtggctcc	aatggggaga	gctaccagaa	300
tgagtgttac	ctgcgacagg	ctgcatgcaa	acagcagagt	gagatacttg	tggtgtcaga	360
aggatcatgt	gccacagtcc	atgaaggctc	tggagaaact	agtcaaaagg	agacatccac	420
ctgtgatatt	tgccagtttg	gtgcagaatg	tgacgaagat	gccgaggatg	tctggtgtgt	480
gtgtaatat	gactgttctc	aaaccaactt	caatcccctc	tgcgcttctg	atgggaaatc	540
ttatgataat	gcatgccaaa	tcaaagaagc	atcgtgtcag	aaacaggaga	aaattgaagt	600
catgtctttg	ggtcgatgtc	aagataacac	aactacaact	actaagtctg	aagatgggca	660
ttatgcaaga	acagattatg	cagagaatgc	taacaaatta	gaagaaagtg	ccagagaaca	720
ccacatacct	tgtccggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
tatcaatatg	caggagccat	cttgcagggtg	tgatgctggg	tatactggac	aacactgtga	840
aaaaaaggac	tacagtgttc	tatacgttgt	tcccggctct	gtacgatttc	agtatgtctt	900
aatcgag						908

<210> 351

<211> 472

<212> DNA

<213> Homo sapien

<400> 351

ccagttat	gcaagtggta	agagcctatt	taccataaat	aatactaaga	accaactcaa	60
gtcaaacctt	aatgccattg	ttattgtgaa	ttaggattaa	gtagtaattt	tcaaaattca	120
cattaacttg	attttaaaat	cagwtttgyg	agtcattttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccattg	tattcctgtt	tttctaaaca	gtcctaattt	ctaactctgt	240
atatactcct	cgacatcaat	gaactttgtt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgccctc	tcaccatgct	ctgctccagg	360
tcagcccccct	tttggcctgt	ttgttttgtc	aaaaacctaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttaggggaag	atgttgcttt	gcccacacac	gaagcaaagt	aa	472

<210> 352

<211> 251

<212> DNA

<213> Homo sapien

<400> 352

114

ctcaaagcta	atctctcggg	aatcaaacca	gaaaagggca	aggatcttag	gcatgggtgga	60
tgtggataag	gccagggtcaa	tggtctgaag	catgcagaga	aagagggtaca	tcggagcggtg	120
caggctgcgt	tccgtcctta	cgatgaagac	cacgatgcag	tttccaaaca	ttgccactac	180
atacatggaa	aggaggggga	agccaaccca	gaaatgggct	ttctctaatac	ctgggatacc	240
aataagcaca	a					251

<210> 353
 <211> 436
 <212> DNA
 <213> Homo sapien

<400> 353						
tttttttttt	tttttttttt	tttttttaca	caatgcagtc	atattatttat	tgagtatgtg	60
cacattatgg	tattattact	atactgatta	tatttatcat	gtgacttcta	attaraaaat	120
gtatccaaaa	gcaaaacagc	agatatataa	aattaaagag	acagaagata	gacattaaca	180
gataaggcaa	cttatacatt	gacaatccaa	atccaatata	tttaaacatt	tgggaaatga	240
gggggacaaa	tggaagccar	atcaaatttg	tgtaaaaacta	ttcagtatgt	ttcccttgct	300
tcatgtctga	raaggctctc	ccttcaatgg	ggatgacaaa	ctccaaatgc	cacacaaatg	360
ttaacagaat	actagattca	cactggaacg	ggggtaaaaga	agaaattatt	ttctataaaa	420
gggtcctctaa	tgtagt					436

<210> 354
 <211> 854
 <212> DNA
 <213> Homo sapien

<400> 354						
ccttttctag	ttcaccagtt	ttctgcaagg	atgctgggta	gggagtgtct	gcaggaggag	60
caagtctgaa	accaaatacta	ggaaacatag	gaaacgagcc	aggcacaggg	ctgggtgggcc	120
atcagggacc	accctttggg	ttgatatttt	gcttaatctg	catcttttga	gtaagatcat	180
ctggcagtag	aagctgttct	ccagggtacat	ttctctagct	catgtacaaa	aacatcctga	240
aggactttgt	caggtgcctt	gctaaaagcc	agatgcgttc	ggcacttcct	tggtctgagg	300
ttaattgcac	acctacaggc	actgggctca	tgctttcaag	tattttgtcc	tcacttttagg	360
gtgagtga	gatccccatt	ataggagcac	ttgggagaga	tcataataaa	gctgactctt	420
gagtacatgc	agtaatgggg	tagatgtgtg	tggtgtgtct	tcatttcctgc	aagggtgctt	480
gttagggagt	gtttccagga	ggaacaagtc	tgaaaccaat	catgaaataa	atggtaggtg	540
tgaactggaa	aactaattca	aaagagagat	cgtgatatca	gtgtgggtga	tacaccttgg	600
caatatggaa	ggctctaatt	tgcccatatt	tgaaataata	attcagcttt	ttgtaataca	660
aaataacaaa	ggattgagaa	tcattggtgc	taattgtataa	aagaccagag	aaacataaat	720
atatcaactg	cataaatgta	aaatgcatgt	gacccaagaa	ggccccaag	tggcagacaa	780
cattgtaccc	attttccctt	ccaaaatgtg	agcggcgggc	ctgctgcttt	caaggctgtc	840
acacgggatg	tcag					854

<210> 355
 <211> 676
 <212> DNA
 <213> Homo sapien

<400> 355						
gaaattaagt	atgagctaaa	ttccctgtta	aaacctctag	gggtgacaga	tctcttcaac	60
caggtcaaaag	ctgatctttc	tggaatgtca	ccaaccaagg	gcctatatatt	atcaaaagcc	120
atccacaagt	catacctgga	tgctcagcaa	gagggcagcg	aggcagcagc	agccactggg	180
gacagcatcg	ctgtaaaaaag	cctaccaatg	agagctcagt	tcaaggcgaa	ccacccttc	240
ctgttcttta	taaggcacac	tcataccaac	acgatcctat	tctgtggcaa	gcttgccctc	300
ccctaatacag	atgggggttg	gtaaggctca	gagttgcaga	tgaggtgcag	agacaatcct	360
gtgactttcc	cacggccaaa	aagctgttca	cacctcacgc	acctctgtgc	ctcagtgttc	420
tcattctgcaa	aataggtcta	ggatttcttc	caaccatttc	atgagttgtg	aagctaaggc	480
tttgtttaatac	atggaaaaag	gtagacttat	gcagaaagcc	tttctggctt	tcttatctgt	540

115

ggtgtctcat	ttgagtgtctg	tccagtgcaca	tgatcaagtc	aatgagtaaa	attttaaggg	600
attagatttt	cttgacttgt	atgtatctgt	gagatcttga	ataagtgacc	tgacatctct	660
gcttaaagaa	aaccag					676

<210> 356
 <211> 574
 <212> DNA
 <213> Homo sapien

<400> 356						
tttttttttt	tttttcagga	aaacattctc	ttactttatt	tgcatctcag	caaaggttct	60
catgtggcac	ctgactggca	tcaaaccaaa	gttcgtaggc	caacaaagat	gggccactca	120
caagcttccc	attttagat	ctcagtgcct	atgagtatct	gacacctgtt	cctctcttca	180
gtctcttagg	gaggcttaaa	tctgtctcag	gtgtgctaag	agtgccagcc	caaggkgttc	240
aaaagtccac	aaaactgcag	tctttgctgg	gatagtaagc	caagcagtgc	ctggacagca	300
gagttctttt	cttgggcaac	agataaccag	acaggactct	aatcgtgctc	ttattcaaca	360
ttcttctgtc	tctgcctaga	ctggaataaa	aagccaatct	ctctcgtggc	acaggggaagg	420
agatacaagc	tcgtttacat	gtgatagatc	taacaaaggc	atctaccgaa	gtctgggtctg	480
gatagacggc	acagggagct	cttaggtcag	cgctgctggg	tggaggacat	tcttgagtcc	540
agctttgcag	cctttgtgca	acagtacttt	ccca			574

<210> 357
 <211> 393
 <212> DNA
 <213> Homo sapien

<400> 357						
tttttttttt	tttttttttt	tttttttttt	tacagaatat	aratgcttta	tcaactgkact	60
taatattgkg	kcttgyttcac	tatacttaaa	aatgcaccac	tcataaatat	ttaattcagc	120
aagccacaac	caaracttga	ttttatcaac	aaaaaccctt	aaatataaac	ggsaaaaaag	180
atagatataa	ttattccagt	ttttttaaaa	cttaaaarat	attccattgc	cgaattaara	240
araarataag	tgttatatgg	aaagaagggc	attcaagcac	actaaaraaa	cctgaggkaa	300
gcataatctg	tacaaaatta	aactgtcctt	tttggcattt	taacaaattt	gcaacgktct	360
tttttttctt	tttctgtttt	tttttttttt	tac			393

<210> 358
 <211> 630
 <212> DNA
 <213> Homo sapien

<400> 358						
acagggtaaa	caggaggatc	cttgctctca	cggagcttac	attctagcag	gaggacaata	60
ttaatgttta	taggaaaatg	atgagtttat	gacaaaggaa	gtagatagtg	ttttacaaga	120
gcatagagta	gggaagctaa	tccagcacag	ggaggtcaca	gagacatccc	taagggaagtg	180
gagtttaaac	tgagagaagc	aagtgcctaa	actgaaggat	gtgttgaaga	agaagggaga	240
gtagaacaat	ttgggcagag	ggaaccttat	agaccctaag	gtgggaaggt	tcaaagaact	300
gaaagagagc	tagaacagct	ggagccgttc	tccggtgtaa	agaggagtca	aagagataag	360
attaaagatg	tgaagattaa	gatccttggtg	gcattcaggg	attggcactt	ctacaagaaa	420
tcaactgaagg	gagtaatgtg	acattacttt	tcaacttcagg	atggccattc	taactccagg	480
gggtagactg	gactaggtaa	gactggaggc	aggtagacct	cttctaaggc	ctgcgatagt	540
gaaagacaaa	aataaagggg	gaaattcagg	ggatagtgaa	aatcagtagg	acttaatgag	600
caagccagag	gttcctccac	aacaaccagt				630

<210> 359
 <211> 620
 <212> DNA
 <213> Homo sapien

116

<400> 359
 acagcattcc aaaatataca tctagagact aarrgtaa at gctctatagt gaagaagtaa 60
 taattaaaaa atgctactaa tatagaaa at ttataatcag aaaaataaat attcagggag 120
 ctccaccagaa gaataaagtg ctctgccagt tattaagga ttactgctgg tgaattaaat 180
 atggcattcc ccaaggga tagagagatt ctctcggatt atgttcaata tttatttcac 240
 aggattaact gttttaggaa cagatataaa gcttcgccac ggaagagatg gacaaagcac 300
 aaagacaaca tgatacctta ggaagcaaca ctaccctttc aggcataaaa tttggagaaa 360
 tgcaacatta tgcttcatga ataatatgta gaaagaaggt ctgatgaaaa tgacatcctt 420
 aatgtaagat aactttataa gaattctggg tcaaataaaa ttctttgaag aaaacatcca 480
 aatgtcattg acttatcaaa tactatcttg gcatataacc tatgaaggca aaactaaaca 540
 aacaaaaagc tcacaccaa caaaaccatc aacttatttt gtattctata acatacgaga 600
 ctgtaaagat gtgacagtgt 620

<210> 360
 <211> 431
 <212> DNA
 <213> Homo sapien

<400> 360
 aaaaaaaaa agccagaaca acatgtgata gataatatga ttggctgcac acttccagac 60
 tgatgaatga tgaacgtgat ggactattgt atggagcaca tcttcagcaa gagggggaaa 120
 tactcatcat ttttgccag cagttgtttg atcaccaa atcatgccag aatactcagc 180
 aaaccttctt agctcttgag aagtcaaagt ccgggggaat ttattcctgg caattttaat 240
 tggactcctt atgtgagagc agcggctacc cagctggggt ggtggagcga acccgctact 300
 agtggacatg cagtggcaga gtccttggt accacctaga ggaatacaca ggcacatgtg 360
 tgatgccaag cgtgacacct gtagcactca aatttgtctt gtttttgtct ttcggtgtgt 420
 agattcttag t 431

<210> 361
 <211> 351
 <212> DNA
 <213> Homo sapien

<400> 361
 aacttgattt ccgatcaaaa gaatcatcat ctttaccttg acttttcagg gaattactga 60
 actttcttct cagaagatag ggcacagcca ttgccttggc ctcaactgaa gggctctgcat 120
 ttgggtctct tggctctctt ccaagtttcc cagccactcg agggagaa atcgggaggt 180
 ttgacttctt ccggggcttt cccgagggct tcaccgtgag ccctgcggcc ctccagggctg 240
 caatcctgga ttcaatgtct gaaacctcgc tctctgctg ctggacttct gaggccgtca 300
 ctgccactct gtctccagc tctgacagct cctcatctgt ggtcctgttg t 351

<210> 362
 <211> 463
 <212> DNA
 <213> Homo sapien

<400> 362
 acttcatcag gccataatgg gtgcctcccg tgagaatcca agcacctttg gactgcgcga 60
 tgtagatgag ccggctgaag atcttgcgca tgcgcggctt cagggcgaag ttcttggcgc 120
 cccgggtcac agaaatgacc aggttgggtg ttttcagggt ccagtgtctg gtcagcagct 180
 cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttccct ttcttcccca 240
 gtgtctcaaa ctgaatatcc ccaaaggcgt cggtaggaaa ttcttgggtg tgtttcttgt 300
 agttccattt ctcaactttg ttgatctggg tgccttccat gtgtcggctc tgggcatagc 360
 cacacttgca cacattctcc ctgataagca cgatgggtgt gacaggaagg aaggatttca 420
 ttgagcctgc ttatggaaac tggattgtt agcttaaata gac 463

<210> 363
 <211> 653

117

<212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(653)
 <223> n = A,T,C or G

<400> 363
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 tgggaggcac tacgcaagat gggactgcgt cctgggggtga gacatcctct ccttgagat 180
 ctaacgaaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc 240
 ccaacagcaa ccccccgaa gtatgagttc ctctrgggcc tccgttccta ccatgagasc 300
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 ctgaggccga agcccggtg gaagcaagaa cccgcattgg aattggagat gaggctgtgt 480
 ntgggccctg gagctgggat gacattgagt ttgagctgct gacctgggat gaggaaggag 540
 attttgaga tccntggtcc agaattccat ttaccttctg ggccagatac caccagaatg 600
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<210> 364
 <211> 401
 <212> DNA
 <213> Homo sapien

<400> 364
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 aaaacaaggt ggatagatct agaattgtaa cattttaaga aaaccatagc atttgacaga 180
 tgagaaagct caattataga tgcaaagtta taactaaact actatagtag taaagaaata 240
 catttcacac ccttcatata aattcactat cttggcttga ggcactccat aaaatgtatc 300
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<210> 365
 <211> 356
 <212> DNA
 <213> Homo sapien

<400> 365
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 taccagagca tcaagtctct gcagcaggtc attcctgggt aaagaaatga cttccacaaa 180
 ctctccatcc cctggctttg gcttcggcct tgcgttttcg gcatcatctc cgtaaatggg 240
 gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga 300
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<210> 366
 <211> 1851
 <212> DNA
 <213> Homo sapien

<400> 366
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 tcaacttctt taagcctttg tgactcttcc tctgatgtca gctttaagtc ttgttctgga 180
 ttgctgtttt cagaagagat ttttaacatc tgtttttctt tgtagtcaga aagtaactgg 240

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<210> 367

<211> 668

<212> DNA

<213> Homo sapien

<400> 367

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accrtataag	agcagtgctt	tggccattaa	tttatctttc	atrttagaca	gcrtagtgya	180
gagtgttatt	tccataactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
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catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
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cgtctgtcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
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<210> 368

<211> 1512

<212> DNA

<213> Homo sapien

<400> 368

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ttcaaacaga	ttggaaaccc	ggagttacct	gctagttggt	gaaactgggt	ggtagacgag	180
atctgttggc	tactactggc	ttctcctggc	tgtaaaaagc	agatgggtgt	tgaggttgat	240
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119

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actccaagaa	aagttaaaca	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagttcc	1440
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<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

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ttcaaacaga	ttggaaaccc	ggagttacct	gctagttggt	gaaactggtt	ggtagacgcg	180
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tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
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120

ccagcctggg tgacagagca agactctgtc tcaaaaaaaaa aaaaaaaaaa aaa 1853

<210> 370
 <211> 2184
 <212> DNA
 <213> Homo sapien

<400> 370
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 tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
 ttattgactt gcctgtgtta gaccggaaga gctgggggtg ttctcaggag ccaccgtgtg 300
 ctgcggcagc ttcgggataa cttgaggctg catcactggg gaagaaacac aytccctgtcc 360
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<210> 371
 <211> 1855
 <212> DNA
 <213> Homo sapien

<220>
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 <223> n = A,T,C or G

<400> 371
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<210> 372

<211> 1059

<212> DNA

<213> Homo sapien

<400> 372

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aatgcacttc	tggtaaatac	ttttgttgaa	aacactgaat	ttgtaaaagg	taatacttac	840
tatttttcaa	tttttccctc	ctaggatttt	tttcccctaa	tgaatgtaag	atggcaaaat	900
ttgcctgaa	ataggtttta	catgaaaact	ccaagaaaag	ttaaacaatg	ttcagtgaat	960
agagatcctg	ctcctttggc	aagttcctaa	aaaacagtaa	tagatacgag	gtgatgcgcc	1020
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<210> 373

<211> 1155

122

<212> DNA

<213> Homo sapien

<400> 373

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agcaacgtgg	gcacttcttg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
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ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tggtgctgcc	actgcttccc	ctgctgcagg	gggagcggca	agagcaaggt	gggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccaggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctggtggggg	aaagtcccca	gaaaggatct	catcgtcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaaga	ggactgctct	acatctggcc	540
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gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcca	ggaagatgaa	660
tgtgcgttaa	tggtgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
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gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
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<210> 374

<211> 2000

<212> DNA

<213> Homo sapien

<400> 374

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ggagactacg	atgacagtgc	cttcatggag	cccaggtacc	acgtccgtgg	agaagatctg	420
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ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaaga	ggactgctct	acatctggcc	540
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123

ctgactaatg	gtgccactgc	tggcaatggt	gatgatggat	taattcctcc	aaggaagagc	1680
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caaaatgata	ctcagaagca	attttgtgaa	gaacagaaca	ctggaatatt	acacgatgag	1800
attctgattc	atgaagaaaa	gcagatagaa	gtggttgaaa	aaatgaattc	tgagctttct	1860
cttagttgta	agaaagaaaa	agacatcttg	catgaaaata	gtacgttgcg	ggaagaaatt	1920
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<210> 375

<211> 2040

<212> DNA

<213> Homo sapien

<400> 375

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ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
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aagcaatttt	gtgaagaaca	gaacactgga	atattacacg	atgagattct	gattcatgaa	1860
gaaaagcaga	tagaagtgg	tgaaaaaatg	aattctgagc	tttctcttag	ttgtaagaaa	1920
gaaaagaca	tcttgcatga	aaatagtacg	ttgcgggaag	aaattgccat	gctaagactg	1980
gagctagaca	caatgaaaca	tcagagccag	ctaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2040

<210> 376

<211> 329

<212> PRT

<213> Homo sapien

<400> 376

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Leu	His	Leu	Ala	Gly	Ser	Asp	Leu	Leu	Ser	Arg	Ser	Leu	Met	Ala	Glu

124

20 25 30
 Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
 35 40 45
 Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
 50 55 60
 Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
 65 70 75 80
 Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
 85 90 95
 Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
 100 105 110
 His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
 115 120 125
 Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
 130 135 140
 Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
 145 150 155 160
 Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
 165 170 175
 Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
 180 185 190
 Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
 195 200 205
 Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
 210 215 220
 Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
 225 230 235 240
 Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
 245 250 255
 Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
 260 265 270
 Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
 275 280 285
 Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
 290 295 300
 Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
 305 310 315 320
 Ser Met Leu Phe Leu Val Ile Ile Met
 325

<210> 377

<211> 148

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(148)

<223> Xaa = Any Amino Acid

<400> 377

Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile
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 Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys
 20 25 30
 Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
 35 40 45
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu

125

50 55 60
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
 65 70 75 80
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
 85 90 95
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
 115 120 125
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
 130 135 140
 Lys Asn Lys Val
 145

<210> 378
 <211> 1719
 <212> PRT
 <213> Homo sapien

<400> 378
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300

Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile
305					310					315					320
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu
				325					330					335	
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val
			340					345					350		
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile
		355					360					365			
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Asn	Val	Ser	Arg	Thr	Arg	Asn	Lys
		370				375					380				
Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser
385					390					395					400
Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys
				405					410					415	
Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly
			420					425					430		
Thr	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys
		435					440					445			
Met	Gly	Lys	Trp	Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly
	450					455					460				
Lys	Ser	Asn	Val	Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys
465				470						475					480
Thr	Leu	Arg	Asn	Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys
				485					490					495	
Cys	Arg	Gly	Ser	Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp
			500					505					510		
Asp	Ser	Ala	Phe	Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu
		515					520					525			
Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp
		530				535					540				
Leu	Ile	Val	Met	Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln
545					550					555					560
Lys	Arg	Thr	Ala	Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val
				565					570					575	
Val	Lys	Leu	Leu	Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn
			580					585					590		
Lys	Lys	Arg	Thr	Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu
		595					600					605			
Cys	Ala	Leu	Met	Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp
		610				615					620				
Glu	Tyr	Gly	Asn	Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys
625					630					635					640
Leu	Met	Ala	Lys	Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys
				645					650					655	
Asn	Lys	His	Gly	Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys
			660					665					670		
Gln	Gln	Val	Val	Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala
		675					680					685			
Leu	Asp	Arg	Tyr	Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly
		690				695					700				
Ser	Ala	Ser	Ile	Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser
705					710					715					720
Ser	Gln	Asp	Leu	Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser
				725					730					735	
His	His	His	Val	Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln
			740					745					750		
Met	Leu	Lys	Ile	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys
		755					760					765			

127

Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser	770	775	780
Gln	Pro	Glu	Lys	Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp	785	790	795
Arg	Glu	Val	Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly		805	810	815
Leu	Leu	Glu	Asn	Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn	820	825	830
Gly	Leu	Ile	Pro	Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe	835	840	845
Pro	Asp	Asn	Glu	Ser	Glu	Glu	Tyr	His	Arg	Ile	Cys	Glu	Leu	Val	Ser	850	855	860
Asp	Tyr	Lys	Glu	Lys	Gln	Met	Pro	Lys	Tyr	Ser	Ser	Glu	Asn	Ser	Asn	865	870	875
Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu	885	890	895
Glu	Gly	Ser	Glu	Asn	Gly	Gln	Pro	Glu	Leu	Glu	Asn	Phe	Met	Ala	Ile	900	905	910
Glu	Glu	Met	Lys	Lys	His	Gly	Ser	Thr	His	Val	Gly	Phe	Pro	Glu	Asn	915	920	925
Leu	Thr	Asn	Gly	Ala	Thr	Ala	Gly	Asn	Gly	Asp	Asp	Gly	Leu	Ile	Pro	930	935	940
Pro	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Ser	Gln	Gln	Phe	Pro	Asp	Thr	Glu	945	950	955
Asn	Glu	Glu	Tyr	His	Ser	Asp	Glu	Gln	Asn	Asp	Thr	Gln	Lys	Gln	Phe	965	970	975
Cys	Glu	Glu	Gln	Asn	Thr	Gly	Ile	Leu	His	Asp	Glu	Ile	Leu	Ile	His	980	985	990
Glu	Glu	Lys	Gln	Ile	Glu	Val	Val	Glu	Lys	Met	Asn	Ser	Glu	Leu	Ser	995	1000	1005
Leu	Ser	Cys	Lys	Lys	Glu	Lys	Asp	Ile	Leu	His	Glu	Asn	Ser	Thr	Leu	1010	1015	1020
Arg	Glu	Glu	Ile	Ala	Met	Leu	Arg	Leu	Glu	Leu	Asp	Thr	Met	Lys	His	1025	1030	1035
Gln	Ser	Gln	Leu	Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met	1045	1050	1055
Pro	Ala	Ala	Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met		1060	1065	1070
Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	1075	1080	1085
Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	1090	1095	1100
Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	1105	1110	1115
Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val	Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	1125	1130	1135
Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn	Lys	Met	Gly	Lys	Trp	Cys	Cys	His	1140	1145	1150
Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	1155	1160	1165
Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe	Met	Glu	Pro	Arg	Tyr	His	Val	Arg	1170	1175	1180
Gly	Glu	Asp	Leu	Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	1185	1190	1195
Pro	Arg	Lys	Asp	Leu	Ile	Val	Met	Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	1205	1210	1215
Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala	Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	1220	1225	1230

Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn
 1235 1240 1245
 Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys
 1250 1255 1260
 Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
 1265 1270 1275 1280
 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
 1285 1290 1295
 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
 1300 1305 1310
 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
 1315 1320 1325
 His Glu Gln Lys Gln Gln Val Lys Phe Leu Ile Lys Lys Lys Ala
 1330 1335 1340
 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
 1345 1350 1355 1360
 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
 1365 1370 1375
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
 1380 1385 1390
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
 1395 1400 1405
 Lys Glu Lys Lys Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
 1410 1415 1420
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
 1425 1430 1435 1440
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
 1445 1450 1455
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
 1460 1465 1470
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
 1475 1480 1485
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
 1490 1495 1500
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
 1505 1510 1515 1520
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
 1525 1530 1535
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
 1540 1545 1550
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
 1555 1560 1565
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
 1570 1575 1580
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
 1585 1590 1595 1600
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
 1605 1610 1615
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
 1620 1625 1630
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
 1635 1640 1645
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
 1650 1655 1660
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
 1665 1670 1675 1680
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
 1685 1690 1695

129

Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
 1700 1705 1710

Met Lys His Gln Ser Gln Leu
 1715

<210> 379

<211> 656

<212> PRT

<213> Homo sapien

<400> 379

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
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 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu

130

370		375		380
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys				
385		390		395
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu				400
		405		410
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn				415
		420		425
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro				430
		435		440
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu				445
		450		455
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu				460
		465		470
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp				475
		485		490
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu				495
		500		505
Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys				510
		515		520
Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly				525
		530		535
Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser				540
		545		550
Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr				555
		565		570
His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln				575
		580		585
Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln				590
		595		600
Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys				605
		610		615
Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile				620
		625		630
Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu				635
		645		650
				655

<210> 380

<211> 671

<212> PRT

<213> Homo sapien

<400> 380

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		20		25
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp				30
		35		40
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp				45
		50		55
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val				60
		65		70
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn				75
		85		90
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser				95
		100		105
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe				110
		115		120
				125

Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His
130						135					140				
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met
145					150					155					160
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala
			165						170					175	
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu
		180					185						190		
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr
	195					200					205				
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met
	210					215					220				
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn
225				230						235					240
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys
			245						250					255	
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly
		260					265						270		
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val
	275					280						285			
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr
	290					295					300				
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile
305				310						315					320
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu
			325						330					335	
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val
		340					345						350		
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile
	355						360					365			
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu
	370					375					380				
Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser	Gln	Pro	Glu	Lys
385				390						395					400
Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp	Arg	Glu	Val	Glu
			405						410					415	
Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly	Leu	Leu	Glu	Asn
		420						425					430		
Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn	Gly	Leu	Ile	Pro
		435					440					445			
Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe	Pro	Asp	Asn	Glu
	450					455					460				
Ser	Glu	Glu	Tyr	His	Arg	Ile	Cys	Glu	Leu	Val	Ser	Asp	Tyr	Lys	Glu
465				470						475					480
Lys	Gln	Met	Pro	Lys	Tyr	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp
			485						490					495	
Leu	Lys	Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu	Glu	Gly	Ser	Glu
		500						505					510		
Asn	Gly	Gln	Pro	Glu	Lys	Arg	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp
	515						520					525			
Gly	Asp	Arg	Glu	Leu	Glu	Asn	Phe	Met	Ala	Ile	Glu	Glu	Met	Lys	Lys
	530					535					540				
His	Gly	Ser	Thr	His	Val	Gly	Phe	Pro	Glu	Asn	Leu	Thr	Asn	Gly	Ala
545				550						555					560
Thr	Ala	Gly	Asn	Gly	Asp	Asp	Gly	Leu	Ile	Pro	Pro	Arg	Lys	Ser	Arg
			565						570					575	
Thr	Pro	Glu	Ser	Gln	Gln	Phe	Pro	Asp	Thr	Glu	Asn	Glu	Glu	Tyr	His
			580					585					590		

132

Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
 595 600 605
 Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
 610 615 620
 Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
 625 630 635 640
 Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
 645 650 655
 Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 660 665 670

<210> 381

<211> 251

<212> DNA

<213> Homo sapien

<400> 381

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 ggtaacatgc ttcccctaag ggtatcccaa cccaggggcc tcaccatgac ctctgagggg 120
 ccaatatccc aggagaagca ttggggaggt gggggcaggt gaaggacca ggactcacac 180
 atcctggggc tccaaggcag aggagagggt cctcaagaag gtcaggagga aaatccgtaa 240
 caagcagtca g 251

<210> 382

<211> 3279

<212> DNA

<213> Homo sapiens

<400> 382

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 cactgggagg ggacatcctg cagaaggtag gaggtagcaa acaccgctg caggggaggg 180
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240
 gggcctggag ggcgtgagga ggagcgaggg ggctgcatgg ctggagttag ggatcagggg 300
 cagggcgcgga gatggcctca cacaggggaag agagggcccc tctgcaggg cctcacctgg 360
 gccacaggag gacactgctt ttcctctgag gagtccaggag ctgtggatgg tgctggacag 420
 aagaaggaca gggcctggct cagggtgtcca gaggctgtcg ctggcttccc tttgggatca 480
 gactgcaggg agggagggcg gcagggttgt ggggggagtg acgatgagga tgacctgggg 540
 gtggetccag gccttggccc tgccctgggc ctcaccagc ctccctcaca gtctctggc 600
 cctcagtctc tcccctccac tccatcctcc atctggcctc agtgggtcat tctgatcact 660
 gaactgacca taccagccc tgcccacggc cctccatggc tcccacatgc cctggagagg 720
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 gcactctgca gatggtccc gcccctatcc tgctgacctg tctgcaggga ctgtccctct 840
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 acacacagca aggttgacgc tgtaaacata gccacgctg tcttggggggc actgggaagc 1740

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ctagataagg ccgtgagcag aaagaagggg aggatcctcc tatgttggtg aaggagggac 1800
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cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920
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cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
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gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtttt 3279

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<210> 383

<211> 154

<212> PRT

<213> Homo sapiens

<400> 383

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Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
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Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
                20              25              30
His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
                35              40              45
Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
                50              55              60
Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
                65              70              75              80
Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
                85              90              95
Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
                100             105             110
Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
                115             120             125
Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
                130             135             140
Ala Leu Glu Arg Gly His Leu Val Arg Glu
145              150

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<210> 384

<211> 557

<212> DNA

<213> Homo sapiens

<400> 384
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 aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
 ggggaagggt cccttttgca ttgccaagt ccataaccat gagcactact ctaccatggg 180
 tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
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 ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480
 tcaattgtga aaatgaatat catgcaaata aattatgcga tttttttttc aaagtaaaaa 540
 aaaaaaaaa aaaaaaa 557

<210> 385
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 385
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 tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
 aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
 tatcagacag gtccagtttc cgcaccaaca cctgctggtt ccctgtcgtg gtctggatct 300
 ctttggccac caattcccc tttccacat cccggca 337

<210> 386
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 386
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 gccgcgtcgg cccagagggt gggcgcgggg ctgcctctac cggctggcgg ctgtaactca 120
 gcgaccttgg cccgaaggct ctagcaagga cccaccgacc ccagccgcgg cggcgggcggc 180
 gcggactttg cccggtgtgt ggggcggagc ggactgctg tccgcggacg ggcagcgaag 240
 atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 387
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 cccctcctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
 tgaaccagga ccggcttctg ggcggtgaa aggggcaagg aggcaaggac ccgtctctc 180
 ccacggatgg ggagagggca ggaggagacc cagccaagt ccttttcctc agcactgagg 240
 gaggggctt gtttccttc cctcccgcg acaagctcca gggcagggt gtccctctgg 300
 gcggcccagc acttcctcag acacaacttc ttctgctgc tccagtcgtg gggatcatca 360
 cttaccacc ccccaagttc aagaccaa atctccagctg ccccttcgt gtttcctgt 420
 gtttgcgtga gctggcatg tctccaggaa ccaagaagcc ctgagcctg tgtagtctcc 480
 ctgaccctt ttaattcctt aagtctaaag atgatgaact tcaaaaaaa aaaaaa 537

<210> 388
 <211> 520
 <212> DNA
 <213> Homo sapiens

135

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<400> 388
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gTTtgAagat tgcctcTTct acagcTTctg agaattgtgt tatttcactt gccAagtGaa 180
ggacccCTc cccaacatgc ccagccac ccctaagcat ggtccCTtgt caccaggcaa 240
ccaggaaact gctactTgtg gacctcacca gagaccagga gggtTtggtt agctcacagg 300
acttcccca cccagaaga ttagcatccc atactagact catactcaac tcaactaggc 360
tcatactcaa ttgatggTTa ttagacaatt ccatttcttt ctggTTatta taaacagaaa 420
atcttctcTc ttctcattac cagtaaaggc tcttggtatc tttctgTTgg aatgatttct 480
atgaactTgt cttattTTaa tggTgggtt ttttctggt 520

```

<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

```

cgTTgccccA gTTtgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagTTaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctcccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgcg ctgctcctcac agctgagact 240
cccaggaaac cttcagacta ccttctctg cttcagcaa ggggcgttg ccacattctc 300
tgagggtcag tgaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

```

<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

```

tgcctctcca tcttggtccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacggnTT ctcatgggtg tgaacatct ctgcttgagg ttccaggaag gcctctggct 120
gctctangag tctganCnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

```

<210> 391

<211> 325

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(325)

<223> n = A,T,C or G

<400> 391

```

tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgccgc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120
tagccagggc actgctgccA acagccagtc cnnataccat catgtnaccc ggtgngctct 180
naantTngat ntccanagcc ctacccatcn tagttctgct ctcccaccgg ntaccagccc 240
cactgccagc gaatcctaca gccagtaccc tgtcccgcag tctctaccta ccagtacgat 300

```

136

gagacctccg gctactacta tgacc

325

<210> 392

<211> 277

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(277)

<223> n = A,T,C or G

<400> 392

```

atattgttta actccttcct ttatatcttt taacattttc atggngaaag gttcacatct 60
agtctcactt nggcnagn gn ctactacttg agtctcttcc ccggcctgnn ccagtngnaa 120
antaccanga accgncatgn cttanaa nccctggtttn tgggttnntc aatgactgca 180
tgacgtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
ctgaggatac agcgccgcgt cctgtgttgc tggggaa 277

```

<210> 393

<211> 566

<212> DNA

<213> Homo sapiens

<400> 393

```

actagtccag tgtggtggaa ttgcgggccg cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacgtt 120
ttgccgggaa cactgcagag acaatgctgt gaggtttccaa ccttagccca tctgcgggca 180
gagaaggtct agtttgtcca tcagcattat catgatatca ggactgggta cttggttaag 240
gagggtctta ggagatctgt cctttttaga gacacottac ttataatgaa gtatttgga 300
gggtgttttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcctttgtt tttgctagtt tgtgttgttg aaaaaaaaaa 480
cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaaa aaaaaa 566

```

<210> 394

<211> 384

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

```

gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaatng gaccgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttta ggagttttta gctgagtgct actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt 384

```

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

```
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgac 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatacagagg ttcatcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggg 360
gcagcctggg gagaccatcc aatcccaaat aaaatgcac 399
```

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

```
tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctacacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataaactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtgagg gataaaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403
```

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

```
actagtnacg tgtggtggaa ttgcggcccg cgtcgacctc naanccatct ctatagcaaa 60
tccatccccg ctcttggttg gtnacagaat gactgacaaa 100
```

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398

```
gcggccgcgt cgacagcagt tccgccagcg ctgcgccctg ggtgggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggaattcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
```

138

ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

<210> 399

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(298)

<223> n = A,T,C or G

<400> 399

acggaggtgg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
ggggtgccng catggagcgc atgggcgcg gcctgggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcatgggc ctggatcatgg accgcatggg ctccgtggag cgcgtgggct 180
ccggcattga gcgcatgggc ccgctgggccc tcgaccacat ggcctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcgtggg 298

<210> 400

<211> 548

<212> DNA

<213> Homo sapiens

<400> 400

acatcaacta ctctctcatt ttaaggtatg gcagttccct tcctcccctt ttcctgcctt 60
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaagggt 120
caaagaacca cagcgttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaagggggc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatcccc 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttggcccca taattctggg cctttgttgt ttgttttaat taactgggca tcccaggaag 420
ctttccagtg atctcctacc atgggcccc ctctgggat caagcccctc ccaggccctg 480
tccccagccc ctctgcccc agcccacccg cttgccttgg tgctcagccc tcccattggg 540
agcaggtt 548

<210> 401

<211> 355

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(355)

<223> n = A,T,C or G

<400> 401

actgtttcca tgttatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60
tgatgtctcc aagtagtcca cttcatitta actctttgaa actgtatcat ctttgccaag 120
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtgcc atgggtggcgg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300
cccttttgca ttgccaaagt ccataaccat gagcactact ctaccatggn tctgc 355

<210> 402

<211> 407

<212> DNA

139

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(407)

<223> n = A,T,C or G

<400> 402

```

atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
tctcacatgc ggtggcatat atagggtcaa aataaaggaa tggagaaaaa tatttcaagc 120
aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180
gaataaagat aaaaaagaga aggacattac aaagggtggtc ctgacctttg ataatctca 240
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa ttgtctgagg 300
ttgtggagct tctccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

```

<210> 403

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 403

```

cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaattc aggcacccaa 60
tctaagcaa gagcctatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
tagagaacaa gacctactca gtcatagaaca aaaaggcaga caccaacatg gatctcatgg 180
gggattggat attgtaatga tagagcagga agatgacagt gatcgctatt tggcacaaca 240
tcttaacaac gaccgaaacc cattattttac ataaacctcc attcggtaac catgttgaaa 300
gga 303

```

<210> 404

<211> 225

<212> DNA

<213> Homo sapiens

<400> 404

```

aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
attgttaatg cactcattta cctttacatg gtgaaagtcc tctcttgatc ctacaaacag 120
acattttcca ctctgttttc catagtgtgt aagtgtatca gatgtgttgg gcatgtgaat 180
ctccaaagtgc ctgtgtaata aataaagtat ctttatttca tttcat 225

```

<210> 405

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(334)

<223> n = A,T,C or G

<400> 405

```

gagctgttat actgtgagtt ctactaggaa atcatcaaatt ctgagggttg tctggaggac 60
ttcaatacac ctccccccat agtgaatcag ctccaggagg gtccagtccc tctccttact 120

```

140

```

tcattcccat cccatgccaa aggaagacc tccctccttg gctcacagcc ttctctaggc 180
ttcccagtcg ctccaggaca gagggggta tgttttcagc tccatccttg ctgtgagtg 240
ctgggtgcgg tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300
cactctccac tctctcanng tggatccac ccct 334

```

```

<210> 406
<211> 216
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

```

```

<400> 406
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216

```

```

<210> 407
<211> 413
<212> DNA
<213> Homo sapiens

```

```

<400> 407
getgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcaccagtg tcagattcta cacctggcca ctcaggaagc aagagttaat 180
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt ttctctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atgggacagg ttctgtagta aag 413

```

```

<210> 408
<211> 183
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(183)
<223> n = A,T,C or G

```

```

<400> 408
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncttaacta gttaatcctt aaagggctan ntaatcctta actagtcctt ccattgtgag 120
cattatcctt ccagtatctn ccttctnttt tatttactcc ttcttggtta cccatgtact 180
ntt 183

```

```

<210> 409
<211> 250
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature

```

141

<222> (1)...(250)

<223> n = A,T,C or G

<400> 409

```

cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtggtttggg ggacctgaac aaacctoctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgcntcctt gctggggggg 240
ggcentatgc                                     250

```

<210> 410

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(306)

<223> n = A,T,C or G

<400> 410

```

ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccagggacc ttggaaacag ttggcactgt aagggtgctt ctccccaaga cacatcctaa 180
aagggtgttg aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
nactggttgg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tcntgc                                     306

```

<210> 411

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(261)

<223> n = A,T,C or G

<400> 411

```

agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaattgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa gngaggcaa a                                     261

```

<210> 412

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(241)

<223> n = A,T,C or G

<400> 412

```

gttcaatgtt acctgacatt tctacaacac cccactcacc gatgtattcg ttgccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgccagg aaatactacg 120

```

142

actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
 ctgggagatt tcaactgggta cattgaattc ccaaactacc cangcaatta cccagccaac 240
 a 241

<210> 413
 <211> 231
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(231)
 <223> n = A,T,C or G

<400> 413
 aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60
 ctcatccaag tttctagtag cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
 aagtttactc tcctcatttg gaacctaaaa actctcttct tcctgggtct gagggctcca 180
 agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414
 <211> 234
 <212> DNA
 <213> Homo sapiens

<400> 414
 actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
 gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
 gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagaggga 180
 ctggaccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca 234

<210> 415
 <211> 217
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(217)
 <223> n = A,T,C or G

<400> 415
 gcataggatt aagactgagt atctttttcta cattctttta acttttctaag gggcactttct 60
 caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cacttttctca 120
 cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
 antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416
 <211> 213
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(213)
 <223> n = A,T,C or G

<400> 416

143

```

atgcatatnt aaagganact gcctcgcttt tagaagacat ctggnotgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag                                     213

```

```

<210> 417
<211> 303
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

```

```

<400> 417
nagtcttcag gccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaata ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
agt                                             303

```

```

<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

```

```

<400> 418
tttttggcgg tgggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcaactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tcctgtgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcaccaat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctgggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgctan gattacaggc cgtgagcc                                     328

```

```

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

```

```

<400> 419
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatattg 60
acccttgagc catggactgg agcctgaaag gcagcgtaca cctgctcct gatcttctgtg 120
cttgtttcct ctctgtggct ccattcatag cacagttgtt gcaactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaccaac ctcaactcgt cccgcaaatt gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtctt ctgctctatc agccatcacg 360

```

144

tggcagccac tcnggctgtg tcgacgcgg

389

<210> 420

<211> 408

<212> DNA

<213> Homo sapiens

<400> 420

```

gttcctccta actcctgcc aaaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attccttgaat gagtctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgcctatg aaaaacctgg caagcccg 408

```

<210> 421

<211> 352

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 421

```

gctcaaaaat ctttttactg atnggcattg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacagggtc tttttgggtc ctctctctcc accacnata acttgacagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacagggtg tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352

```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```

atgccaccat gctggcaatg cagcgggagg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcgcgcg cgtcaatcct ggccaaggct agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggtc 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttcg cgggtacggc tggcctatga aaattat 337

```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(310)

<223> n = A,T,C or G

<400> 423

145

```

gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggccctggcct gggagccctg tgcctactan aagcncatta gattatccat 120
tcaactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagttaa                                     310

```

<210> 424

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(370).

<223> n = A,T,C or G

<400> 424

```

gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaaatc cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaagggt gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg                                     370

```

<210> 425

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(216)

<223> n = A,T,C or G

<400> 425

```

aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaatga 60
taacaacnca acatcaaggc aananaaca ggaatggntg actntgcata aatnggccga 120
anattatcca ttaatntaag ggttgacttc aggntacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtnttntg aggagg                                     216

```

<210> 426

<211> 596

<212> DNA

<213> Homo sapiens

<400> 426

```

cttccagtga ggataaccct gttgccccgg gccgaggttc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gcccgaaggg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggtga 180
gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggccca ttaagaggca cttcccgtta 300
ttaggcagtt catctgcact gataacttct tggcagctga gctggctgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agceaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540
gtcccgtggt tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct      596

```

146

<210> 427
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(107)
 <223> n = A,T,C or G

<400> 427
 gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncaccag 60
 cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng 107

<210> 428
 <211> 38
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(38)
 <223> n = A,T,C or G

<400> 428
 gaacttcna anaangactt tattcactat ttacatt 38

<210> 429
 <211> 544
 <212> DNA
 <213> Homo sapiens

<400> 429
 ctttgctgga cggaataaaa gtggacgcaa gcatgaccto ctgatgaggg cgctgcattt 60
 attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
 atatccacga actcttgaag gactttctga ttatccaca atcaaatacat cggttttcag 180
 tttggatggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
 gccttccact tcagttacac ctactcacc atcctctcct gttggttctg tgetgcttca 300
 agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
 tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420
 gagttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
 acctcaaca gttagagaga tatgcatatc cagggatttt ttgccaggtg gtaggagaga 540
 ttat 544

<210> 430
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(507)
 <223> n = A,T,C or G

<400> 430
 cttatcncaa tggggctccc aaacttggtt gtgcagtgga aactccgggg gaattttgaa 60
 gaacactgac acccatcttc caccgccaga ctctgattta attgggctgc agtgagaaca 120

147

```

gagcatcaat ttaaaaagct gccagaatg ttntcctggg cagcgttggt atctttgcn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcggtgt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagttaa tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcttc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa 507

```

```

<210> 431
<211> 392
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

```

```

<400> 431
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattatct gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240
catcattcca gcattctgag attaggngga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttggttag taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggctttttac tctgctgttt ct 392

```

```

<210> 432
<211> 387
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(387)
<223> n = A,T,C or G

```

```

<400> 432
ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctoggna gtccagccac tngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgott ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtag aggaccggga 360
acaacgtata gaacactgga gtccttt 387

```

```

<210> 433
<211> 281
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(281)
<223> n = A,T,C or G

```

```

<400> 433
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60

```

148

```

ctgattaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagnagg ntctctgtnt gccactggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

```

<210> 434

<211> 484

<212> DNA

<213> Homo sapiens

<400> 434

```

ttttaaaata agcatttagt gctcagtcct tactgagtag tctttctctc cctcctctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatatgt 120
tggtgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaacat ttcaccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaacc 360
tgctccaatc tgctacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
ttaa 484

```

<210> 435

<211> 424

<212> DNA

<213> Homo sapiens

<400> 435

```

gcgcgctca gagcaggtea ctttctgcct tccacgtcct ctttcaagga agcccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaaccct ctcctcgcct gacttcggaa ctggcgagag ttcagcgag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcattggtc ggggtgacc 240
cttggagaga ggaaaaaggg cacaagagg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaacctct ggactcccca tgccttaact cccacactct 360
gctatcagaa acttaaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac 424

```

<210> 436

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(667)

<223> n = A, T, C or G

<400> 436

```

accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataaggggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggacggtg tagcaactga tcttcagaaa gaggaactgt gtgcacggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccagggttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatatc tctttcttat atactctcca 420
agttcataat gctgctccat gccagctggg gtgagttggc caaatccttg tggcatgag 480
gattccttta tggggtcagt gggaaagggt tcaatgggac ttcggtctcc atgctgaaac 540
accaaagtca caaacttcaa ctcttgggt agtacacttc ggtctagcca gaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660

```

tgttgag

667

<210> 437

<211> 693

<212> DNA

<213> Homo sapiens

<400> 437

```

ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaaag ctggattggc acactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtaactct ctattttcac cctcttgcct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatggt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcaact ttggggggac agccagcatc tttagctttc 420
atttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaaact gctgttgctc ctgaggtggt gaaagacaga tatagagctt acagtattta 540
tctatattct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc

```

693

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

```

ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac ctctgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctgggtg agaagaagga ccaaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

```

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

```

gttcctnnta actcctgcc aaaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtgtg tgactttgggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat ggtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t

```

431

<210> 440

<211> 523

<212> DNA

<213> Homo sapiens

150

<400> 440

```

agagataaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcttggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta 523

```

<210> 441

<211> 430

<212> DNA

<213> Homo sapiens

<400> 441

```

gttcctccta actcctgcc aaaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggt tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctggggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attccttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcgcccgcg 420
aatttagtag 430

```

<210> 442

<211> 362

<212> DNA

<213> Homo sapiens

<400> 442

```

ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcttgtaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

```

<210> 443

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(624)

<223> n = A,T,C or G

<400> 443

```

ttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaacac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360

```

151

```

taacgcctac aaaacactta aacatagata acatagggtgc aagtactatg tatctgggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga ggggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatac                                     624

```

<210> 444

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(425)

<223> n = A,T,C or G

<400> 444

```

gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgtg gtcagcaaata ccttgaatgc 180
tgcttaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacacctg gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggctgcag cggccgcgaa tttagtagta 420
gtaga                                     425

```

<210> 445

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 445

```

catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcatgtggc agattattgg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtgggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggcctctcc tcttgtattt tgaagcagtg 360
tgggtgctgg attgataaaa aaaaaaaaaa tcgacgcggc cgcaattta gtag 414

```

<210> 446

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(631)

<223> n = A,T,C or G

<400> 446

```

acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120

```

152

```

atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggctcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtgggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg catttggtgt 540
aatctacacc aatgaaaaca tgtactacag ctatatttga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g                                     631

```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

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ccttgaggaaa antntcacia tataaagggt cgtagacttt actccaaatt ccaaaaaggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgcagacacc ttctggggga aacagggtcg 300
ccagggttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttettata tactctecaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcgggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggtta gtacacttcg gtcta                                     585

```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```

tgctcgtggg tcattctgan nncgaaactg acctgcccag ccctgccgan gggccnccat 60
ggctccctag tgccctggag agganggggc tag                                     93

```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(706)

<223> n = A,T,C or G

<400> 449

```

ccaagttcat gctntgtgct ggacgctgga cagggggcaa aagcnnttgc tcgtgggtca 60

```

153

```

ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtcctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggctcggcg cgtcccattc gccattcagg ctgcgcaact 240
gttgggaagg gcgatcgggt cgggcctctt cgctattacg ccagctggcg aaaggggat 300
gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcncga cgttgtaaaa 360
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cgtacgtaag cttggatcct ctagagcggc cgctactac tactaaattc gcggccgcgt 480
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aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncacca 660
gcatggatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa 706

```

```

<210> 450
<211> 493
<212> DNA
<213> Homo sapiens

```

```

<400> 450
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acagttttta aaggtaaaac aacataaaaa gaaatcct atagtggaaa taagagagtc 120
aaatgaggct gagaacttta caaagggatc ttacagacat gtgcgaata tcaactgcatg 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
caagtcagggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360
tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480
gcgaatttag tag 493

```

```

<210> 451
<211> 501
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

```

```

<400> 451
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ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtogcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
cgcncagac actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420
gttgcaatga gctgagatca ggccnctgcn cccagcatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a 501

```

```

<210> 452
<211> 51
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(51)
<223> n = A,T,C or G

```

154

<400> 452
 agacgggtttc accntttacaa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453
 <211> 317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (317)
 <223> n = A,T,C or G

<400> 453
 tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
 acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatggttc tcagaaccat 120
 ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180
 taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
 cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
 taccatgtc tttatta 317

<210> 454
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 454
 ttcgaggtag aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60
 taagccacgc cagctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120
 agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180
 ctttcctttt tcagtgttcc aaagctcctc acaatttcac gaacaacagc t 231

<210> 455
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 455
 taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60
 cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
 gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180
 caaagaattt ctcatagcac agctcacaat acagggtctc tttctcctct a 231

<210> 456
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 456
 ttggcaggta ccocttataaa gaagacacca taccttatgc gttattaggt ggaataatca 60
 ttccattcag tattatcggtt attattcttg gagaaaccct gtctgtttac tgtaaccttt 120
 tgactcaaaa ttcctttatc aggaataact acatagccac tatttataaa gccattggaa 180
 cttttttatt tgggtgcagct gctagtcagt cctgactga cattgccaaag t 231

<210> 457
 <211> 231
 <212> DNA

155

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 457

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cgaggtaccc aggggtctga aaatctctnn tttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catcacagttt 120
tatttgatgtt tatttagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
agttgtctaa atcgatgcct catttctctt gaggtgtcgc tggcttttgt g 231
```

<210> 458

<211> 231

<212> DNA

<213> Homo sapiens

<400> 458

```
aggtctggtt cccccactt ccactcccct ctactctctc taggactggg ctgggccaaag 60
agaagagggg tgggttaggga agccgttgag acctgaagcc ccaccctcta ccttccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggctctgggt taggcatttt gggggggccag accccaggag aagaagattc t 231
```

<210> 459

<211> 231

<212> DNA

<213> Homo sapiens

<400> 459

```
ggtaccgagg ctgcgtgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtgggt gcccaccagt cctaacggga caggacagag agacagagca 120
gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231
```

<210> 460

<211> 231

<212> DNA

<213> Homo sapiens

<400> 460

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gcaggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231
```

<210> 461

<211> 231

<212> DNA

<213> Homo sapiens

<400> 461

```
cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggaggggc 60
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120
gtgggggttca gtgaggagtg ggaaattggg tcagcagaac caagccgttg ggtgaataag 180
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231
```

<210> 462

156

<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

```

aggtagcctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggttag tgggttagag atttccagag tcttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

```

<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

<400> 463

```

tactccagcc tggtagacaga gggagaccct atcaccgccc cccacccccc caaaaaaaaa 60
actgagtaga caggtgtcct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cggtgtcccc atctgagtga gaaaaggcag 180
tggtgaggtg gatcttccag tcgaagcggg atagaagccc gtgtgaaaag c 231

```

<210> 464

<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

```

gtactctaag attttatcta agttgccttt tctgggtggg aaagttaaac cttagtgaact 60
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 120
cctgttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
gggtgccagc caccagctag atgctctgta acttctaggg cccattttcc c 231

```

<210> 465

<211> 231

<212> DNA

<213> Homo sapiens

<400> 465

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catgttggtg tagctgtggg aatgctggct gcatctcaga cagggttaac ttcagctcct 60
gtggcaaatt agcaacaaat tctgacatca tatattatgt ttctgtatct ttgttgatga 120
aggatggcac aatttttggc tgtgttcata atatactcag attagtccag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgttgtagc tctggtaatg a 231

```

<210> 466

<211> 231

<212> DNA

<213> Homo sapiens

<400> 466

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caggtacctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacaat ttgccaggga 120
cctgtgcaat caaatattgt ggagaattcc ctagctggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgcgggt g 231

```

<210> 467

<211> 311

<212> DNA

<213> Homo sapiens

<400> 467

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gtacaccctg gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg 60
tgggtggcttt tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac 120
tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
gcatgggtct ctgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240
tgtgacctgc tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga 300
ctgcagcaga c                                     311

```

<210> 468

<211> 3112

<212> DNA

<213> Homo sapiens

<400> 468

```

catttgtgttg ggagaaaaac agagggggaga ttttgtgtggc tgcagccgag ggagaccagg 60
aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
tggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaaggc 180
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<210> 469

<211> 2229

<212> DNA

<213> Homo sapiens

<400> 469

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tgatttgcca	aaattctaaa	gcgcactcac	catgaaatgg	ataaagggtta	cctttgggga	180
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ctaaaaatac	aaaaattagc	tgggcgtgct	ggtgcatgcc	tgtaatccca	gccccaacac	2220
aatggaatt						2229

<210> 470

<211> 2426

<212> DNA

<213> Homo sapiens

<400> 470

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<211> 812

<212> DNA

<213> Homo sapiens

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160

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812

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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<400> 472

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515

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<212> DNA

<213> Homo sapiens

<400> 473

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162

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 <211> 1594
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
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 <223> n=A, T, C or G

<400> 475

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<210> 476
 <211> 3434
 <212> DNA
 <213> Homo sapiens

<400> 476

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tgccaagagg  gcagccacag  gtcattctta  ggaggacttt  atgttccagt  ccagaaagca  180
gccagtggta  ccacccagg  gacttgtgct  tctgtggccc  aggccagacg  tagaatttga  240
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```

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```

<210> 477
 <211> 140
 <212> PRT
 <213> Homo sapiens

165

<400> 477

```

Met Asp Gly His Thr Asp Ile Trp Arg Asn His Met Asp Thr Pro Pro
      5              10              15
His Tyr His Arg Asp Thr Asp Thr Arg Arg His His His Met Asp Thr
      20              25              30
Leu Ser His Tyr His Arg Asp Thr Arg His His Thr Val Thr Trp Thr
      35              40              45
His His His Thr His Glu His Thr Asp Thr Leu Pro Tyr Gly His Trp
      50              55              60
His Thr His Cys His Thr Val Thr Trp Thr His Leu His Thr Ile Thr
      65              70              75              80
Pro Pro His Thr Leu Pro Val Asp Thr Arg Thr His Arg His Cys His
      85              90              95
Thr Asp Thr Gln Asn Thr Val Thr Arg Arg His His His Ala Asp Thr
      100             105             110
Pro Pro Leu Trp Cys Arg Leu Asn Tyr Pro Ala Gly Gly Thr Ala Val
      115             120             125
Ala Tyr Ser Cys Leu Ser Asp Trp Leu Ser Pro Gln
      130             135             140

```

<210> 478

<211> 143

<212> PRT

<213> Homo sapiens

<400> 478

```

Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
      5              10              15
Ser His Gly His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
      20              25              30
Gly Glu Ile Thr Trp Thr His His His Thr Ile Thr Gly Thr Gln Thr
      35              40              45
His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
      50              55              60
Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
      65              70              75              80
Pro Thr His Cys His Met Asp Thr Gly Thr His Thr Ala Thr Leu Ser
      85              90              95
His Gly His Thr Ser Thr Pro Ser His His His Thr His Cys Leu Trp
      100             105             110
Thr Gln Gly His Thr Asp Thr Val Thr Gln Ile His Lys Thr Leu Ser
      115             120             125
His Gly Asp Ile Thr Met Gln Ile His His His Ser Gly Ala Val
      130             135             140

```

<210> 479

<211> 222

<212> PRT

<213> Homo sapiens

<400> 479

```

Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
      5              10              15
Ser His Glu His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
      20              25              30

```

166

Gly Glu Ile Thr Leu Thr His His His Thr Ile Thr Gly Thr Gln Thr
 35 40 45
 His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
 50 55 60
 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
 65 70 75 80
 Pro Thr His Cys His Met Asp Thr Ala Thr His Thr Ala Thr Leu Ser
 85 90 95
 His Gly His Thr Ser Ile Pro Ser His His His Thr His Cys His Val
 100 105 110
 Asp Thr Arg Thr His Arg His Cys His Thr Asp Thr Gln Asn Thr Val
 115 120 125
 Thr Arg Arg His His His Ala Asp Thr Pro Pro His Gly His Ser Thr
 130 135 140
 Arg His Ser Ala Thr Gln Ile His His His Thr Glu Met Arg Thr His
 145 150 155 160
 Cys His Thr Asp Thr Thr Thr Ser Leu Pro His Phe His Val Ser Ala
 165 170 175
 Gly Gly Val Gly Pro Thr Thr Leu Gly Ser Asn Arg Glu Ile Thr Trp
 180 185 190
 Thr Tyr Ser Glu Gly Lys Ile Phe Phe Tyr Phe Leu Gly Asn Gln Ala
 195 200 205
 Arg Leu Cys Leu Lys Lys Arg Lys Lys Lys Gln Tyr Thr Val
 210 215 220

<210> 480
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 480
 Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val
 5 10 15
 Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr
 20 25 30
 Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg
 35 40 45
 Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly
 50 55 60
 Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln
 65 70 75 80
 Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys
 85 90 95
 Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly
 100 105 110
 Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu
 115 120 125
 Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly
 130 135 140

<210> 481
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 481

167

```

Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro
      5              10              15
Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg
      20              25              30
Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser
      35              40              45
Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys
      50              55              60
Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro
      65              70              75              80
Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser Ser Trp Arg
      85              90              95
Ala Leu Ala Glu Val Thr Gly Cys Ser Leu Gly Pro Leu Gly Leu Ala
      100             105             110
Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys Trp Ser His
      115             120             125
Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr Ala Ala Phe
      130             135             140
Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu Trp Ala Ser
      145             150             155             160
Trp Leu Ser Arg Gly Arg Pro
      165

```

<210> 482

<211> 143

<212> PRT

<213> Homo sapiens

<400> 482

```

Met Glu Pro Tyr Arg Gly Asn Lys Lys Gln Val Gln Glu Lys Gly Val
      5              10              15
Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
      20              25              30
Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
      35              40              45
Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
      50              55              60
Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe
      65              70              75              80
Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
      85              90              95
Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
      100             105             110
Ala Ser Gly Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
      115             120             125
Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly
      130             135             140

```

<210> 483

<211> 143

<212> PRT

<213> Homo sapiens

<400> 483

```

Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val
      5              10              15
Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala

```

168

20 25 30
 Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
 35 40 45
 Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
 50 55 60
 Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
 65 70 75 80
 Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
 85 90 95
 Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
 100 105 110
 Arg Leu Val Gln Ala Glu His Pro Pro His Pro Leu Glu Glu Val
 115 120 125
 Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
 130 135 140

<210> 484
 <211> 30
 <212> PRT
 <213> Homo Sapien

<400> 484
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
 20 25 30

<210> 485
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 485
 gggaagctta tcacctatgt gccgcctctg c

31

<210> 486
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 486
 gcgaattctc acgctgagta tttggcc

27

<210> 487
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 487

169

cccggaattct tagctgccca tccgaacgcc ttcac

36

<210> 488
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 488

gggaagcttc ttccccggct gcaccagctg tgc

33

<210> 489
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 489

Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
1 5 10 15
Ser Val Ala

<210> 490
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 490

Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
1 5 10 15
Leu Ser His Ser
20

<210> 491
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 491

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Leu
1 5 10 15
Thr Gly Phe Thr
20

<210> 492
<211> 20
<212> PRT

170

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 492

Ala	Leu	Thr	Gly	Phe	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr
1				5					10					15	
Leu	Ala	Ser	Leu												
			20												

<210> 493

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 493

Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro
1				5					10					15	
Lys	Tyr	Arg	Gly												
			20												

<210> 494

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 494

Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala	Ser	Ser	Glu	Asp	Ser
1				5					10					15	
Leu	Met	Ile	Ser												
			20												

<210> 495

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 495

Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro	Gly	Ala	Pro
1				5					10					15	
Phe	Pro	Asn	Gly												
			20												

<210> 496

<211> 21

<212> PRT

<213> Artificial Sequence

171

<220>

<223> Made in a lab

<400> 496

Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
1 5 10 15
Pro Pro Pro Pro Ala
20

<210> 497

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 497

Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
1 5 10 15
Ser Val Arg Val
20

<210> 498

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 498

Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val
1 5 10 15
Val Pro Gly Arg
20

<210> 499

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 499

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
1 5 10 15
Ser Ala Phe Leu
20

<210> 500

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

172

<223> Made in a lab

<400> 500

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Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
 1           5           10           15
Gly Ser Ile Val
                20

```

<210> 501

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 501

```

Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met
 1           5           10           15
Val Ser Ala Ala
                20

```

<210> 502

<211> 414

<212> DNA

<213> Homo Sapien

<220>

<221> misc_feature

<222> (1)...(414)

<223> n=A,T,C or G

<400> 502

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caccatggag acaggcctgc gctggctttt cctggtcgct gtgetcaaag gtgtccaatg      60
tcagtcgggtg gaggagtcct ggggtcgctt ggtcacgcct gggacacctt tgacantcac      120
ctgtagagatt tttggaatng acctcagtag caatgcaatg agctgggtcc gccagggtcc      180
aggggaagggg ctggaatgga tcggagccat tgataattgt ccacantacg cgacctgggc      240
gaaaggccga ttnatnattt ccaaaacctn gaccacggtg gatttgaaaa tgaccagtcc      300
gacaaccgag gacacggcca cctatttttg tggcagaatg aatactggta atagtggttg      360
gaagaatatt tggggcccag gcaccctggt caccgtntcc tcagggaac ctaa          414

```

<210> 503

<211> 379

<212> DNA

<213> Homo Sapien

<220>

<221> misc_feature

<222> (1)...(379)

<223> n=A,T,C or G

<400> 503

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atnccatgggt gcttgggtcaa aggtgtccag tgtcagtcgg tggaggagtc cgggggtcgc      60
ctgggtcacgc ctgggacacc cctgacactc acctgcaccg tntctggatt ngacatcagt      120
agctatggag tgagctgggt ccgccaggct ccagggaagg ggctggnata catcggatca      180
ttagtagtag tggtagattt tacgcgagct gggcgaaagg ccgattcacc atttccaaaa      240
cctngaccac ggtggatttg aaaatcacca gtttgacaac cgaggacacg gccacctatt      300
tntgtgccag aggggggttt aattataaag acatttgggg cccaggcacc ctggtcaccg      360

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173

tntccttagg gcaacctaa

379

<210> 504
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 504
 Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Glu
 1 5 10 15
 Asn Ser Ala

<210> 505
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 505
 Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn Asp Asn Val Thr
 1 5 10 15
 Asn Thr Ala Asn
 20

<210> 506
 <211> 407
 <212> DNA
 <213> Homo Sapien

<400> 506
 atggagacag gcctgcgctg gcttctcctg gtcgctgctg tcaaagggtg ccagtgtcag 60
 tcgctggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgc 120
 accgtctctg gattctccct cagtagcaat gcaatgatct gggcccgcca ggctccaggg 180
 aaggggctgg aatacatcgg atacattagt tatgggtgga gcgcatacta cgcgagctgg 240
 gtgaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctgag aatgaccagt 300
 ctgacaaccg aggacacggc cacctatttc tgtgccagaa atagtgattt tagtggtatg 360
 ttgtggggcc caggcacctt ggtcacctgc tcctcagggc aacctaa 407

<210> 507
 <211> 422
 <212> DNA
 <213> Homo Sapien

<400> 507
 atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaagggtg ccagtgtcag 60
 tcggtggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgt 120
 acagtctctg gattctccct cagcaactac gacctgaact gggcccgcca ggctccaggg 180
 aaggggctgg aatggatcgg gatcattaat tatgttgga ggacggacta cgcgaactgg 240
 gcaaaaggcc gggtcaccat ctccaaaacc tcgaccacgg tggatctcaa gatcgccagt 300
 ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagtct 360
 ggtccgtgct tgcgcactct gggcccaggc accctgggtc cgtctcctt agggcaacct 420

174

aa

422

<210> 508
 <211> 411
 <212> DNA
 <213> Homo Sapien

<220>
 <221> misc_feature
 <222> (1)...(411)
 <223> n=A,T,C or G

<400> 508
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 cgggtggagga gtccgggggt cgcttggtca cgcttgggac acccctgaca ctacacctgca 120
 cagtctctgg aatcgacctc agtagctact gcatgagctg ggtccgccag gctccagga 180
 aggggctgga atggatcgga atcattggta ctcttggtga cacatactac gcgaggtggg 240
 cgaaaggccg attcaccatc tccaaaacct cgaccacggt gcatntgaaa atcnccagtc 300
 cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta 360
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<210> 509
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 509
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 1 5 10 15

<210> 510
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 510
 Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile
 1 5 10 15

<210> 511
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 511

Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln Lys
 1 5 10 15

175

<210> 512
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 512
 Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu
 1 5 10 15

<210> 513
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 513
 Ala Pro Cys Gly Gln Val Gly Val Pro Asx Val Tyr Thr Asn Leu
 1 5 10 15

<210> 514
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 514
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 1 5 10 15

<210> 515
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 515
 Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg
 1 5 10 15

<210> 516
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 516
 Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln

176

1 5 10 15
 <210> 517
 <211> 15
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

 <400> 517
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met
 1 5 10 15

 <210> 518
 <211> 15
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

 <400> 518
 Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 1 5 10 15

 <210> 519
 <211> 17
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

 <400> 519
 Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg Asn Tyr Asp Glu Gly Cys
 1 5 10 15
 Gly

 <210> 520
 <211> 25
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Made in a lab

 <400> 520
 Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr
 1 5 10 15
 Glu Ala Arg Arg His Tyr Asp Glu Gly
 20 25

 <210> 521
 <211> 21
 <212> PRT
 <213> Artificial Sequence

177

<220>

<223> Made in a lab

<400> 521

Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu
1				5					10					15	
Pro	Pro	Pro	Pro	Ala											
				20											

<210> 522

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 522

Leu	Leu	Val	Val	Pro	Ala	Ile	Lys	Lys	Asp	Tyr	Gly	Ser	Gln	Glu	Asp
1				5					10					15	
Phe	Thr	Gln	Val												
			20												

<210> 523

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<220>

<221> VARIANT

<222> (1)...(254)

<223> Xaa = any amino acid

<400> 523

Met	Ala	Thr	Ala	Gly	Asn	Pro	Trp	Gly	Trp	Phe	Leu	Gly	Tyr	Leu	Ile
1				5					10					15	
Leu	Gly	Val	Ala	Gly	Ser	Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile
			20					25					30		
Asn	Gly	Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu
		35				40						45			
Val	Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln
	50				55					60					
Trp	Val	Leu	Ser	Ala	Thr	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly
65					70				75					80	
Leu	Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met
			85					90						95	
Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu
			100					105					110		
Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu
		115					120				125				
Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala
	130					135				140					
Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg
145					150					155					160

178

Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
 165 170 175
 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
 180 185 190
 Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly
 195 200 205
 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
 210 215 220
 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
 225 230 235 240
 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 245 250

<210> 524
 <211> 765
 <212> DNA
 <213> Homo sapien

<400> 524
 atggccacag caggaaatcc ctggggctgg ttcctggggg acctcatcct tgggtgtcgca 60
 ggatcgctcg tctctggtag ctgcagccaa atcataaacg gcgaggactg cagcccgcac 120
 tcgcagccct ggcaggcggc actgggtcatg gaaaacgaat tgttctgctc gggcgctcctg 180
 gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcgagg 240
 ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc 300
 ctctccgtac ggcacccaga gtacaacaga cccttgctcg ctaacgacct catgtctatc 360
 aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag 420
 tgccctaccg cgggggaactc ttgectcggt tctggctggg gtctgctggc gaacggcaga 480
 atgcctaccg tgctgcagtg cgtgaacgtg tcgggtggtg ctgaggagggt ctgcagtaag 540
 ctctatgacc cgctgtacca cccagcatg ttctgcgccg gcggaggggca agaccagaag 600
 gactcctgca acgggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt 660
 gtgtctttcg gaaaagcccc gtgtggccaa gttggcgtgc cagggtgtcta caccaacctc 720
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<210> 525
 <211> 254
 <212> PRT
 <213> Homo sapien

<400> 525
 Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
 1 5 10 15
 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
 20 25 30
 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
 35 40 45
 Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
 50 55 60
 Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
 65 70 75 80
 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
 85 90 95
 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
 100 105 110
 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
 115 120 125
 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
 130 135 140
 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg

179

145		150		155		160									
Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Glu
			165					170						175	
Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys
			180					185					190		
Ala	Gly	Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly
		195					200					205			
Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly
	210					215					220				
Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu
225					230					235					240
Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser		
			245						250						

<210> 526

<211> 963

<212> DNA

<213> Homo sapiens

<400> 526

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aactgcatcg tgggtcttcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180
tttctctgca tgcttgacgc cattgacctg gccttatcca catccaccat gcctaagatc 240
cttgcccttt tctgggttga ttcccgagag attagctttg aggcctgtct taccagatg 300
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gcccagattg gcatcgtggc tgtgggtcgc ggatccctct tttttttccc actgcctctg 480
ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540
caggatgtaa tgaagttggc ctatgcagac actttgccca atgtggtata tggcttact 600
gccattctgc tgggtcatggg cgtggacgta atgttcatct ccttgtccta ttttctgata 660
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caccgctttg gaaacagcct tcatccatt gtgcgtgttg tcatgggtga catctacctg 840
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<210> 527

<211> 320

<212> PRT

<213> Homo sapiens

<400> 527

Met	Ser	Ser	Cys	Asn	Phe	Thr	His	Ala	Thr	Phe	Val	Leu	Ile	Gly	Ile
				5					10					15	
Pro	Gly	Leu	Glu	Lys	Ala	His	Phe	Trp	Val	Gly	Phe	Pro	Leu	Leu	Ser
		20						25					30		
Met	Tyr	Val	Val	Ala	Met	Phe	Gly	Asn	Cys	Ile	Val	Val	Phe	Ile	Val
	35					40					45				
Arg	Thr	Glu	Arg	Ser	Leu	His	Ala	Pro	Met	Tyr	Leu	Phe	Leu	Cys	Met
	50				55					60					
Leu	Ala	Ala	Ile	Asp	Leu	Ala	Leu	Ser	Thr	Ser	Thr	Met	Pro	Lys	Ile
	65				70				75					80	
Leu	Ala	Leu	Phe	Trp	Phe	Asp	Ser	Arg	Glu	Ile	Ser	Phe	Glu	Ala	Cys
		85					90						95		
Leu	Thr	Gln	Met	Phe	Phe	Ile	His	Ala	Leu	Ser	Ala	Ile	Glu	Ser	Thr
	100						105						110		

180

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
 130 135 140
 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
 145 150 155 160
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
 180 185 190
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
 210 215 220
 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
 245 250 255
 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
 260 265 270
 Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
 275 280 285
 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
 290 295 300
 Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
 305 310 315 320

<210> 528
 <211> 20
 <212> DNA
 <213> Homo Sapien

<400> 528
 actatggtcc agaggctgtg

20

<210> 529
 <211> 20
 <212> DNA
 <213> Homo Sapien

<400> 529
 atcacctatg tgccgcctct

20

<210> 530
 <211> 1852
 <212> DNA
 <213> Homo sapiens

<400> 530
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 tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180
 tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
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 tgatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga 540

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ttgggtaggt  tccaccatgt  tgccgcagat  gacatgattt  cagtacctgt  gtctggctga  600
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gctttctcca  ccttgctgga  agtgacctgc  tgtccagaag  tttgatggct  gaggagtata  720
ccatcgtgca  tgcattcttc  atttcctgca  tttcttcctc  cctggatgga  cagggggagc  780
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aacgtggtcg  cttggggaga  ctacgatgac  agcgcttca  tggatcccag  gtaccacgtc  960
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gcgaatttaa  atgcgctgga  tagatatgga  agaactgctc  tcataactgc  tgtatgttgt  1500
ggatcagcaa  gtatagtcag  ccctctactt  gagcaaaatg  ttgatgtatc  ttctcaagat  1560
ctggaaagac  ggccagagag  tatgctgttt  ctatgcatca  tcatgtaatt  tgccagttac  1620
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aagacttaaa  gctgacatca  gaggaagagt  cacaaaggct  taaaggaagt  gaaaacagcc  1740
agccagagct  agaagattta  tggctattga  agaagaatga  agaacacgga  agtactcatg  1800
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<210> 531

<211> 879

<212> DNA

<213> Homo sapiens

<400> 531

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tgcaagtggg  gctgccactg  cttccctctg  tgcaggggga  gcggcaagag  caacgtggct  180
gcttggggag  actacgatga  cagcgcttct  atggatccca  ggtaccacgt  ccatggagaa  240
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ctggcctctg  ccaatgggaa  ttcagaagta  gtaaaactcg  tgctggacag  acgatgtcaa  420
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<210> 532

<211> 292

<212> PRT

<213> Homo sapiens

<400> 532

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Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
      5              10              15
Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
      20              25              30
Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
      35              40              45
Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp

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182

50	55	60
Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu		
65	70	75
Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg		80
	85	90
Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp		95
	100	105
Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser		110
	115	120
Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu		125
	130	135
Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu		140
	145	150
Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile		155
	165	170
Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu		175
	180	185
Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu		190
	195	200
Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu		205
	210	215
Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu		220
	225	230
Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys		235
	245	250
Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp		255
	260	265
Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu		270
	275	280
Val Ile Ile Met		285
290		

<210> 533
 <211> 801
 <212> DNA
 <213> Homo sapiens

<400> 533
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 tatgccactg cagcattcct gggtgccaaag aggccaaacca caggccatct tgagaaggag 180
 tttatgttcc actgcagaaa gcagccagga tcaccatcca ggggacttgg tcttctgtgg 240
 cctggccag acatagaatt tgtgccaaag caggacaagc tcactcagag cagcgtgtta 300
 gtacctcaaa tctgtgcgtg ccagacaagg ccaaactggc tcaatgagca accagccacc 360
 tctgcagggg tgcgtctgga ggaggtggac cagccacca ccttaccag tcaagggaagt 420
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 ttaggaaaag cagatggccc ttggccctac ctttttggtta gaagaactga tgttccatgt 540
 cctgcagcga gtgaggttgg tggctgtgcc ccagctcct ggcacaccct cgcagaggtg 600
 actggttgct ctttgagccc ttttagcctt gccagcatg cacaagcctc agtgcacta 660
 ctgtgctaca aatggagcca tatagggaac acgagcagcc atctcaggag caaggtgtat 720
 gctgcctttg ggggtccag tccttgccctc aagggtotta tgtcactgtg ggcttcttgg 780
 ttgccaagag gcagaccata g 801

<210> 534
 <211> 266
 <212> PRT
 <213> Homo sapiens

183

<400> 534

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Met Tyr Lys Leu Gln Cys Asn Asn Cys Ala Thr Asn Gly Ala Thr Glu
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Arg Lys Gln Ala Ala Gly Ser Gly Ala Gly Tyr Ala Leu Pro Ser Ala
      20      25      30
Leu Gln Ser Met Pro Gln Gly Ser Tyr Ala Thr Ala Arg Phe Leu Val
      35      40      45
Ala Lys Arg Pro Thr Thr Gly His Leu Glu Lys Glu Phe Met Phe His
      50      55      60
Cys Arg Lys Gln Pro Gly Ser Pro Ser Arg Gly Leu Gly Leu Leu Trp
      65      70      75      80
Pro Trp Pro Asp Ile Glu Phe Val Pro Arg Gln Asp Lys Leu Thr Gln
      85      90      95
Ser Ser Val Leu Val Pro Gln Ile Cys Ala Cys Gln Thr Arg Pro Asn
      100      105      110
Trp Leu Asn Glu Gln Pro Ala Thr Ser Ala Gly Val Arg Leu Glu Glu
      115      120      125
Val Asp Gln Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys
      130      135      140
Ser His Ser Leu Ser Gly Cys His Leu Met Ala Asp Ile Ala Lys Ala
      145      150      155      160
Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr
      165      170      175
Asp Val Pro Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser
      180      185      190
Ser Trp His Thr Leu Ala Glu Val Thr Gly Cys Ser Leu Ser Pro Leu
      195      200      205
Ser Leu Ala Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys
      210      215      220
Trp Ser His Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr
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Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
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Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
                    65                      70                      75                      80
Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
                    85                      90                      95
Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
                    100                     105                     110
Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
                    115                     120                     125
Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
                    130                     135                     140
Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
                    145                     150                     155                     160
Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
                    165                     170                     175

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188

Lys	Ala	Leu	Arg	Leu	Ser	Asn	Met	Ala	Met	Gly	Lys	Thr	Thr	Thr	Gly
		180						185						190	
Gln	Ile	Val	Asn	Leu	Leu	Ser	Asn	Asp	Val	Asn	Lys	Phe	Asp	Gln	Val
		195					200					205			
Thr	Val	Phe	Leu	His	Phe	Leu	Trp	Ala	Gly	Pro	Leu	Gln	Ala	Ile	Ala
	210				215					220					
Val	Thr	Ala	Leu	Leu	Trp	Met	Glu	Ile	Gly	Ile	Ser	Cys	Leu	Ala	Gly
225					230					235					240
Met	Ala	Val	Leu	Ile	Ile	Leu	Leu	Pro	Leu	Gln	Ser	Cys	Phe	Gly	Lys
			245						250					255	
Leu	Phe	Ser	Ser	Leu	Arg	Ser	Lys	Thr	Ala	Thr	Phe	Thr	Asp	Ala	Arg
		260						265					270		
Ile	Arg	Thr	Met	Asn	Glu	Val	Ile	Thr	Gly	Ile	Arg	Ile	Ile	Lys	Met
		275					280					285			
Tyr	Ala	Trp	Glu	Lys	Ser	Phe	Ser	Asn	Leu	Ile	Thr	Asn	Leu	Arg	Lys
	290				295						300				
Lys	Glu	Ile	Ser	Lys	Ile	Leu	Arg	Ser	Ser	Cys	Leu	Arg	Gly	Met	Asn
305					310					315					320
Leu	Ala	Ser	Phe	Phe	Ser	Ala	Ser	Lys	Ile	Ile	Val	Phe	Val	Thr	Phe
			325						330					335	
Thr	Thr	Tyr	Val	Leu	Leu	Gly	Ser	Val	Ile	Thr	Ala	Ser	Arg	Val	Phe
		340					345						350		
Val	Ala	Val	Thr	Leu	Tyr	Gly	Ala	Val	Arg	Leu	Thr	Val	Thr	Leu	Phe
	355						360					365			
Phe	Pro	Ser	Ala	Ile	Glu	Arg	Val	Ser	Glu	Ala	Ile	Val	Ser	Ile	Arg
	370				375						380				
Arg	Ile	Gln	Thr	Phe	Leu	Leu	Leu	Asp	Glu	Ile	Ser	Gln	Arg	Asn	Arg
385					390					395					400
Gln	Leu	Pro	Ser	Asp	Gly	Lys	Lys	Met	Val	His	Val	Gln	Asp	Phe	Thr
			405					410						415	
Ala	Phe	Trp	Asp	Lys	Ala	Ser	Glu	Thr	Pro	Thr	Leu	Gln	Gly	Leu	Ser
		420						425					430		
Phe	Thr	Val	Arg	Pro	Gly	Glu	Leu	Leu	Ala	Val	Val	Gly	Pro	Val	Gly
	435					440						445			
Ala	Gly	Lys	Ser	Ser	Leu	Leu	Ser	Ala	Val	Leu	Gly	Glu	Leu	Ala	Pro
	450				455						460				
Ser	His	Gly	Leu	Val	Ser	Val	His	Gly	Arg	Ile	Ala	Tyr	Val	Ser	Gln
465				470						475					480
Gln	Pro	Trp	Val	Phe	Ser	Gly	Thr	Leu	Arg	Ser	Asn	Ile	Leu	Phe	Gly
		485						490						495	
Lys	Lys	Tyr	Glu	Lys	Glu	Arg	Tyr	Glu	Lys	Val	Ile	Lys	Ala	Cys	Ala
		500						505					510		
Leu	Lys	Lys	Asp	Leu	Gln	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Thr	Val	Ile
		515					520					525			
Gly	Asp	Arg	Gly	Thr	Thr	Leu	Ser	Gly	Gly	Gln	Lys	Ala	Arg	Val	Asn
	530					535					540				
Leu	Ala	Arg	Ala	Val	Tyr	Gln	Asp	Ala	Asp	Ile	Tyr	Leu	Leu	Asp	Asp
545					550					555					560
Pro	Leu	Ser	Ala	Val	Asp	Ala	Glu	Val	Ser	Arg	His	Leu	Phe	Glu	Leu
			565						570					575	
Cys	Ile	Cys	Gln	Ile	Leu	His	Glu	Lys	Ile	Thr	Ile	Leu	Val	Thr	His
		580						585					590		
Gln	Leu	Gln	Tyr	Leu	Lys	Ala	Ala	Ser	Gln	Ile	Leu	Ile	Leu	Lys	Asp
		595					600					605			
Gly	Lys	Met	Val	Gln	Lys	Gly	Thr	Tyr	Thr	Glu	Phe	Leu	Lys	Ser	Gly
	610					615					620				
Ile	Asp	Phe	Gly	Ser	Leu	Leu	Lys	Lys	Asp	Asn	Glu	Glu	Ser	Glu	Gln
625					630					635					640

Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
 645 650 655
 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
 660 665 670
 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
 675 680 685
 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
 690 695 700
 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
 705 710 715 720
 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
 725 730 735
 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
 740 745 750
 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr
 755 760 765
 Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu
 770 775 780
 Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys
 785 790 795 800
 Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn
 805 810 815
 Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu
 820 825 830
 Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu
 835 840 845
 Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile
 850 855 860
 Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg
 865 870 875 880
 Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr
 885 890 895
 Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp
 900 905 910
 Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp
 915 920 925
 Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr
 930 935 940
 Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val
 945 950 955 960
 Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala
 965 970 975
 Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met
 980 985 990
 Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile
 995 1000 1005
 Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro
 1010 1015 1020
 Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val
 1025 1030 1035 1040
 Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu
 1045 1050 1055
 Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly
 1060 1065 1070
 Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu
 1075 1080 1085
 Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu
 1090 1095 1100

190

Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile
 1105 1110 1115 1120
 Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp
 1125 1130 1135
 Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu
 1140 1145 1150
 Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr
 1155 1160 1165
 Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu
 1170 1175 1180
 Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile
 1185 1190 1195 1200
 Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln
 1205 1210 1215
 Lys Lys Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys
 1220 1225

<210> 538

<211> 1261

<212> PRT

<213> Homo sapiens

<400> 538

Met Tyr Ser Val Leu Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu
 5 10 15
 Leu Gln Gly Phe Trp Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala
 20 25 30
 Gln Lys Pro Ser Leu Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser
 35 40 45
 Tyr Leu Val Leu Gly Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val
 50 55 60
 Ile Gln Pro Ile Phe Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr
 65 70 75 80
 Asp Pro Met Asp Ser Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr
 85 90 95
 Val Leu Thr Phe Cys Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr
 100 105 110
 Phe Tyr His Val Gln Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys
 115 120 125
 His Met Ile Tyr Arg Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly
 130 135 140
 Lys Thr Thr Thr Gly Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn
 145 150 155 160
 Lys Phe Asp Gln Val Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro
 165 170 175
 Leu Gln Ala Ile Ala Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile
 180 185 190
 Ser Cys Leu Ala Gly Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln
 195 200 205
 Ser Cys Phe Gly Lys Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr
 210 215 220
 Phe Thr Asp Ala Arg Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile
 225 230 235 240
 Arg Ile Ile Lys Met Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile
 245 250 255
 Thr Asn Leu Arg Lys Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys
 260 265 270
 Leu Arg Gly Met Asn Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile

		275					280					285			
Val	Phe	Val	Thr	Phe	Thr	Thr	Tyr	Val	Leu	Leu	Gly	Ser	Val	Ile	Thr
	290					295					300				
Ala	Ser	Arg	Val	Phe	Val	Ala	Val	Thr	Leu	Tyr	Gly	Ala	Val	Arg	Leu
305					310						315				320
Thr	Val	Thr	Leu	Phe	Phe	Pro	Ser	Ala	Ile	Glu	Arg	Val	Ser	Glu	Ala
				325					330					335	
Ile	Val	Ser	Ile	Arg	Arg	Ile	Gln	Thr	Phe	Leu	Leu	Leu	Asp	Glu	Ile
			340					345					350		
Ser	Gln	Arg	Asn	Arg	Gln	Leu	Pro	Ser	Asp	Gly	Lys	Lys	Met	Val	His
		355					360					365			
Val	Gln	Asp	Phe	Thr	Ala	Phe	Trp	Asp	Lys	Ala	Ser	Glu	Thr	Pro	Thr
	370					375						380			
Leu	Gln	Gly	Leu	Ser	Phe	Thr	Val	Arg	Pro	Gly	Glu	Leu	Leu	Ala	Val
385					390					395					400
Val	Gly	Pro	Val	Gly	Ala	Gly	Lys	Ser	Ser	Leu	Leu	Ser	Ala	Val	Leu
				405						410				415	
Gly	Glu	Leu	Ala	Pro	Ser	His	Gly	Leu	Val	Ser	Val	His	Gly	Arg	Ile
			420					425					430		
Ala	Tyr	Val	Ser	Gln	Gln	Pro	Trp	Val	Phe	Ser	Gly	Thr	Leu	Arg	Ser
		435					440					445			
Asn	Ile	Leu	Phe	Gly	Lys	Lys	Tyr	Glu	Lys	Glu	Arg	Tyr	Glu	Lys	Val
	450					455					460				
Ile	Lys	Ala	Cys	Ala	Leu	Lys	Lys	Asp	Leu	Gln	Leu	Leu	Glu	Asp	Gly
465					470					475					480
Asp	Leu	Thr	Val	Ile	Gly	Asp	Arg	Gly	Thr	Thr	Leu	Ser	Gly	Gly	Gln
				485					490					495	
Lys	Ala	Arg	Val	Asn	Leu	Ala	Arg	Ala	Val	Tyr	Gln	Asp	Ala	Asp	Ile
			500					505					510		
Tyr	Leu	Leu	Asp	Asp	Pro	Leu	Ser	Ala	Val	Asp	Ala	Glu	Val	Ser	Arg
		515					520					525			
His	Leu	Phe	Glu	Leu	Cys	Ile	Cys	Gln	Ile	Leu	His	Glu	Lys	Ile	Thr
	530					535					540				
Ile	Leu	Val	Thr	His	Gln	Leu	Gln	Tyr	Leu	Lys	Ala	Ala	Ser	Gln	Ile
545					550					555					560
Leu	Ile	Leu	Lys	Asp	Gly	Lys	Met	Val	Gln	Lys	Gly	Thr	Tyr	Thr	Glu
				565					570					575	
Phe	Leu	Lys	Ser	Gly	Ile	Asp	Phe	Gly	Ser	Leu	Leu	Lys	Lys	Asp	Asn
			580					585					590		
Glu	Glu	Ser	Glu	Gln	Pro	Pro	Val	Pro	Gly	Thr	Pro	Thr	Leu	Arg	Asn
		595					600					605			
Arg	Thr	Phe	Ser	Glu	Ser	Ser	Val	Trp	Ser	Gln	Gln	Ser	Ser	Arg	Pro
	610					615									

				740				745					750			
Thr	Leu	His	Asn	Lys	Met	Phe	Glu	Ser	Ile	Leu	Lys	Ala	Pro	Val	Leu	
		755					760					765				
Phe	Phe	Asp	Arg	Asn	Pro	Ile	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys	
	770					775					780					
Asp	Ile	Gly	His	Leu	Asp	Leu	Leu	Pro	Leu	Thr	Phe	Leu	Asp	Phe	800	
785					790					795						
Ile	Gln	Thr	Leu	Leu	Gln	Val	Val	Gly	Val	Val	Ser	Val	Ala	Val	Ala	
			805						810						815	
Val	Ile	Pro	Trp	Ile	Ala	Ile	Pro	Leu	Val	Pro	Leu	Gly	Ile	Ile	Phe	
			820						825					830		
Ile	Phe	Leu	Arg	Arg	Tyr	Phe	Leu	Glu	Thr	Ser	Arg	Asp	Val	Lys	Arg	
		835					840					845				
Leu	Glu	Ser	Thr	Thr	Arg	Ser	Pro	Val	Phe	Ser	His	Leu	Ser	Ser	Ser	
	850					855					860					
Leu	Gln	Gly	Leu	Trp	Thr	Ile	Arg	Ala	Tyr	Lys	Ala	Glu	Glu	Arg	Cys	
865					870										880	
Gln	Glu	Leu	Phe	Asp	Ala	His	Gln	Asp	Leu	His	Ser	Glu	Ala	Trp	Phe	
			885						890						895	
Leu	Phe	Leu	Thr	Thr	Ser	Arg	Trp	Phe	Ala	Val	Arg	Leu	Asp	Ala	Ile	
			900					905						910		
Cys	Ala	Met	Phe	Val	Ile	Ile	Val	Ala	Phe	Gly	Ser	Leu	Ile	Leu	Ala	
	915						920						925			
-Lys	Thr	Leu	Asp	Ala	Gly	Gln	Val	Gly	Leu	Ala	Leu	Ser	Tyr	Ala	Leu	
	930					935						940				
Thr	Leu	Met	Gly	Met	Phe	Gln	Trp	Cys	Val	Arg	Gln	Ser	Ala	Glu	Val	
945					950					955					960	
Glu	Asn	Met	Met	Ile	Ser	Val	Glu	Arg	Val	Ile	Glu	Tyr	Thr	Asp	Leu	
				965						970					975	
Glu	Lys	Glu	Ala	Pro	Trp	Glu	Tyr	Gln	Lys	Arg	Pro	Pro	Pro	Ala	Trp	
			980.					985					990			
Pro	His	Glu	Gly	Val	Ile	Ile	Phe	Asp	Asn	Val	Asn	Phe	Met	Tyr	Ser	
		995					1000					1005				
Pro	Gly	Gly	Pro	Leu	Val	Leu	Lys	His	Leu	Thr	Ala	Leu	Ile	Lys	Ser	
	1010					1015						1020				
Gln	Glu	Lys	Val	Gly	Ile	Val	Gly	Arg	Thr	Gly	Ala	Gly	Lys	Ser	Ser	
1025					1030						1035				1040	
Leu	Ile	Ser	Ala	Leu	Phe	Arg	Leu	Ser	Glu	Pro	Glu	Gly	Lys	Ile	Trp	
				1045						1050					1055	
Ile	Asp	Lys	Ile	Leu	Thr	Thr	Glu	Ile	Gly	Leu	His	Asp	Leu	Arg	Lys	
			1060					1065						1070		
Lys	Met	Ser	Ile	Ile	Pro	Gln	Glu	Pro	Val	Leu	Phe	Thr	Gly			

				1205					1210					1215			
Val	Leu	Leu	Gln	Asn	Lys	Glu	Ser	Leu	Phe	Tyr	Lys	Met	Val	Gln	Gln		
			1220					1225					1230				
Leu	Gly	Lys	Ala	Glu	Ala	Ala	Ala	Leu	Thr	Glu	Thr	Ala	Lys	Gln	Arg		
		1235					1240					1245					
Trp	Gly	Phe	Thr	Met	Leu	Ala	Arg	Leu	Val	Ser	Asn	Ser					
	1250					1255					1260						

<400> 543
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val
5 10

<400> 544

Met Thr

<400> 545

Ser Val

<400> 546

Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
20 25

<400> 547

Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Pro	Cys	Arg	Ala	Arg	Leu
			20					25				30		
Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His	Gln	Leu
		35					40					45		Cys
Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu					
	50					55								

<400> 548

Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu

	5	10	15
Glu Cys			
<210>	549		
<211>	18		
<212>	PRT		
<213>	Homo sapiens		
<400>	549		
Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg			
	5	10	15
Gln Ala			

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<210> 550
<211> 14
<212> PRT
<213> Homo sapiens
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<400> 550
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe
5 10

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<210> 551
<211> 11
<212> PRT
<213> Artificial Sequence
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<220>
<223> Made in a lab

<400> 551
 Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 5 10

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<210> 552
<211> 2577
<212> DNA
<213> Homo sapiens
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INSDOCID: <WO_____0173032A2 1 >

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<400> 553
Ser Ile Cys Asn Met Thr Cys Ala Ser Val Phe Phe Cys Asp Gln Lys
                    5                      10                      15
Phe Leu Thr Phe Ser Phe Leu Ser Met Val Glu Pro Pro Arg Ala Gly
                    20                      25                      30
Val Leu Asn Ser Gln Ala Thr Asp Ser Tyr Gln Ser Thr Asp Tyr Tyr
                    35                      40                      45
Glu Pro His His Thr Gly Gly Gly Glu His
                    50                      55

```

```

<400> 554
Leu Gln Lys Asn Lys Leu Arg Ala Ser Thr Asp Ser Thr Leu Trp Ile
              5              10              15
Cys Ala Ala Glu Ala Ser Thr Lys Pro Tyr Phe Tyr Thr Cys Leu Val
              20              25              30
Met Leu His Gly Gln Gly Leu Ala Leu Leu Ser Pro Thr Asn Leu Pro
              35              40              45
Glu Ile Leu Arg Phe Leu Phe Asn Gly Phe Leu
      50              55

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197

<210> 555
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 555
 Leu Gly Arg Phe Ser Leu Ser Cys Lys Ser Gly His Ser Arg Gly Gln
 5 10 15
 Pro Gln Leu Gly Ala Thr Ala Gln Gly Lys Val His Met Gly Leu Ser
 20 25 30
 Thr Ala Gln Gly Ser Ile Gln Asp Ile Lys Val Pro His Ser Ile Asp
 35 40 45
 Leu Val Ala Lys Lys Lys Lys Gln Thr Leu Ile Ser Phe Cys His Pro
 50 55 60
 Ser Asp Pro Leu Glu Leu Leu
 65 70

<210> 556
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 556
 Asn His Pro Glu Gln Gly Ser Ser Thr Pro Arg Pro Gln Thr His Thr
 5 10 15
 Ser Pro Arg Thr Ile Met Asn His Thr Thr Gln Glu Glu Val Ser Thr
 20 25 30
 Arg Gln Ala Lys Glu Ala Ser Pro Val Leu Thr Ala Thr Arg His Gly
 35 40 45
 Ser Tyr Tyr Ser Leu Asn Ser Ala Ser Thr Gln Ile Ser Asp Asn Ile
 50 55 60
 Arg Asn Ser Leu Glu His Glu Pro Cys Cys Glu Leu Pro Ile Arg Arg
 65 70 75 80
 Ile

<210> 557
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 557
 Ser Leu Ser Ala Thr Pro Leu Thr Leu Trp Asn Ser Ser Asp Pro Leu
 5 10 15
 Glu Gln Ala Tyr Leu Ile Ser Ala Arg Glu Lys Thr Asn Asn Gly Leu
 20 25 30
 Lys Gly Ser Leu Thr Met Lys Val Ser Ala Asn Ser Trp Leu Arg Cys
 35 40 45
 Gly Phe His Ile Arg Phe
 50

<210> 558
 <211> 77
 <212> PRT
 <213> Homo sapiens

198

<220>

<221> VARIANT

<222> (1)...(77)

<223> Xaa = Any amino acid

<400> 558

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Asn Asp Arg Asp Arg Asn Ser Asn Lys Val Ile Xaa Lys Ala Asn Leu
              5              10              15
Ile Tyr Phe Thr Asn Leu Thr Ser Cys Leu Ser Val Gln Asn Gln Thr
              20              25              30
Phe Thr Cys Thr Lys Arg His Lys His Leu Gln Cys Ser Ser Val His
              35              40              45
Leu Cys Lys Ile Pro Pro Arg Leu Lys Gly Arg Asp Lys Lys Lys Lys
              50              55              60
Pro Ser Tyr Leu Ser Gly Val Leu His Ser Arg Ser Tyr
              65              70              75

```

<210> 559

<211> 50

<212> PRT

<213> Homo sapiens

<400> 559

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Thr Leu Pro Pro Leu Arg Ser Val Ile Thr Leu Glu Thr His Trp Ser
              5              10              15
Thr Asn Pro Val Val Asn Cys Leu Ser Glu Gly Ser Arg Leu Cys Ala
              20              25              30
Ser Tyr Glu Asn Leu Met Pro Asp Leu Ser Leu Ser His Phe Ala
              35              40              45
Pro Arg
              50

```

<210> 560

<211> 56

<212> PRT

<213> Homo sapiens

<400> 560

```

Ile Gly Ser Leu Lys Gly Pro Thr Thr Ala Gly Ser His Cys Ser Gly
              5              10              15
Glu Gly Ser Tyr Gly Thr Phe Tyr Cys Pro Arg Phe Tyr Thr Gly Tyr
              20              25              30
Lys Gly Ala Ser Gln Tyr Arg Ser Gly Ser Lys Glu Glu Glu Thr Asn
              35              40              45
Thr Asp Leu Phe Leu Pro Pro Leu
              50              55

```

<210> 561

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

199

<222> (1)...(57)

<223> Xaa = Any amino acid

<400> 561

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Val Leu His Leu Asp Gln Met Asn Asn Val Gly Ile Xaa Met Asp Lys
      5              10              15
Gly Leu Lys Ser Pro Glu Ile Lys Asn Pro Ala Pro Thr Gly Thr Ser
      20              25              30
Asn Leu Ser Cys Phe Leu Ser Xaa Phe Trp Leu Met Gln Gly Thr Asn
      35              40              45
Ser Leu Pro Arg Glu Asn Tyr Leu Asn
      50              55

```

<210> 562

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(59)

<223> Xaa = Any amino acid

<400> 562

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Asp Leu Tyr Pro Xaa Arg Ser Gln His Cys Ser Phe Asp Pro Ser Val
      5              10              15
Ala Pro Met His Gly Ile Lys Asn Ser Ile Thr Ser Leu Ile Phe Leu
      20              25              30
Ile Ser Tyr Leu Xaa Leu Glu Met Ser Ser Leu Ser Glu Ser Leu Val
      35              40              45
Leu Ser Ser Gly Asp Tyr Val Leu Asp Thr Pro
      50              55

```

<210> 563

<211> 79

<212> PRT

<213> Homo sapiens

<400> 563

```

Cys Phe Leu Phe Pro Tyr Leu Trp Leu Tyr Ala Gln Pro Leu Phe Pro
      5              10              15
Lys Gln Gln Pro Pro Ala Leu Ala Pro Gly His Pro Asp Phe Ile His
      20              25              30
Thr Gln Asn Glu Gln Ile Asp Pro Ser Pro His Ile Gln Asn Leu Met
      35              40              45
Trp Asn Pro His Leu Ser Gln Glu Leu Ala Glu Thr Phe Met Val Arg
      50              55              60
Asp Pro Leu Arg Pro Leu Leu Val Phe Ser Leu Ala Asp Ile Arg
      65              70              75

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<210> 564

<211> 64

<212> PRT

<213> Homo sapiens

<400> 564

200

Ala Cys Ser Lys Gly Ser Glu Glu Phe Gln Arg Val Arg Gly Val Ala
 5 10 15
 Glu Arg Asp Gln Cys Leu Phe Leu Leu Leu Cys Tyr Gln Ile Tyr Thr
 20 25 30
 Val Arg His Leu Tyr Ile Leu Tyr Arg Thr Leu Gly Ser Arg Lys Ser
 35 40 45
 His Met Asn Leu Pro Leu Ser Ser Gly Ser Gln Leu Trp Leu Ala Pro
 50 55 60

<210> 565

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(57)

<223> Xaa.= Any amino acid

<400> 565

Leu Tyr Tyr Cys Ser Tyr Leu Cys His Phe Arg Thr Ala Leu Ile Leu
 5 10 15
 Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
 20 25 30
 Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu
 35 40 45
 Tyr Ala Val Ser Ser Xaa His Asn Val
 50 55

<210> 566

<211> 55

<212> PRT

<213> Homo sapiens

<400> 566

Ile Leu Leu Glu Phe Phe Arg Asn Gln Arg Gly Ser Leu Asn Pro Arg
 5 10 15
 Lys Thr Val Pro Phe Ile Lys Ser Glu Gly Gly Glu Lys Lys Gly His
 20 25 30
 Cys Asn His Ser Val Val Ser Ile Asp Ser Ala Ala Ala Leu Leu Pro
 35 40 45
 Leu Lys Leu Val Leu Leu Pro
 50 55

<210> 567

<211> 51

<212> PRT

<213> Homo sapiens

<400> 567

Tyr Ser Asp Phe Asp Val Phe Cys Ser His Thr Tyr Gly Tyr Met Leu
 5 10 15
 Ser His Cys Ser Gln Ser Ser Ser Pro Leu Leu Trp Pro Leu Gly Ile
 20 25 30
 Leu Thr Leu Ser Thr His Lys Met Ser Lys Leu Thr Leu Pro Pro Ile

201

35
Phe Arg Thr
50

40

45

<210> 568
<211> 75
<212> PRT
<213> Homo sapiens

<400> 568
Lys Val Gly Glu Tyr Ile Leu Gln Ser Leu Leu Arg Ile Arg Lys Ile
5 10 15
Tyr Val Ala Phe Asn Ser Val Pro Ser Thr Cys Leu Leu Ala Ser Leu
20 25 30
Thr Glu Thr Pro Val Thr Thr Ile Leu Thr Ile Ile Ile Asn Leu Thr
35 40 45
Cys Phe Gln His Ala Glu Ser Ser Tyr Leu Phe Tyr Pro Leu Ala Asp
50 55 60
Phe Leu Leu Gln His Ile Ser Leu Gly Lys Leu
65 70 75

<210> 569
<211> 4809
<212> DNA
<213> Homo sapiens

<400> 569
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<210> 570
 <211> 951
 <212> DNA
 <213> Homo sapiens

<400> 570

203

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ccatttttagt actatgggtg agtacatgga attgaagtct ggcttaaatac ttcagaaagt 180
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<210> 571

<211> 819

<212> DNA

<213> Homo sapiens

<400> 571

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accagcctgg ccaacatggt gaaatcccg ttcactaaaa atacaaaaat taccaggga 600
tggtggcggg cgctgtaat cccaggtaact cgggaggctg agggaggaga atcgcttgaa 660
cctgggaggg tgagggagga gaatcgcttg aaccggggag gcagagggtg cagtgaaccg 720
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aaataaacia acaaaacaaac aaaacagaga gattttgct 819

```

<210> 572

<211> 203

<212> DNA

<213> Homo sapiens

<400> 572

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tatagaatac tcaagctatg catcaagctt ggtaccgagc tcggatccac tatttacggc 60
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attgtgttgg gcccaacaca atggagccac cacatccagc ctgccacata cttttaact 180
atcaggtctc atgagaactc atg 203

```

<210> 573

<211> 132

<212> PRT

<213> Homo sapiens

<400> 573

```

Met Val Glu Gly Glu Gly Glu Ala Arg His Val Leu His Gly Gly Arg
          5              10              15
Arg Glu Arg Val Arg Gly Glu Thr Ala Thr Asn Phe Phe Phe Leu Arg

```

204

```

      20      25      30
Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu
      35      40      45
Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu
      50      55      60
Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala
      65      70      75      80
Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly
      85      90      95
Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro
      100      105      110
Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile
      115      120      125
Leu Leu Asn Tyr
      130

```

<210> 574
 <211> 62
 <212> PRT
 <213> Homo sapiens

```

<400> 574
Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn
      5      10      15
His Gly Gly Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln
      20      25      30
Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
      35      40      45
Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
      50      55      60

```

<210> 575
 <211> 76
 <212> PRT
 <213> Homo sapiens

```

<400> 575
Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp
      5      10      15
Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu
      20      25      30
Ser Leu Glu Pro Gly Arg Leu Arg Glu Asn Arg Leu Asn Pro Gly
      35      40      45
Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
      50      55      60
Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
      65      70      75

```

<210> 576
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT

205

<222> (1)...(68)

<223> Xaa = Any Amino Acid

<400> 576

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Met Leu Gly Lys Ser Arg Ala Val Cys Leu Pro Ser Thr Thr Val Thr
              5              10              15
Thr Val Cys Tyr Leu Ala Ser Ser Ser Ala Ser Arg Glu Thr Ala Thr
              20              25              30
Arg Gln Ala Pro Gly Asn Trp Lys Met Xaa Ser Lys Cys His Ala Gln
              35              40              45
Leu Leu Phe Thr Phe Tyr Leu Asn His Phe Tyr Gln Ile Arg Leu Asn
              50              55              60
Pro Gly Tyr Ser
65

```

<210> 577

<211> 57

<212> PRT

<213> Homo sapiens

<400> 577

```

Met Tyr Leu Glu Asn Ser Phe Tyr Cys Gln Met Ile Leu Leu Lys Arg
              5              10              15
Cys Arg Leu Ser Lys Ile Ser Thr Gln Arg Val Val Pro Asp Gly Pro
              20              25              30
Pro Ala Pro Val Pro Gly Ser Phe Pro Met Phe Pro Arg Phe Gly Phe
              35              40              45
Arg Leu Ala Pro Pro Ala Asp Thr Pro
              50              55

```

<210> 578

<211> 51

<212> PRT

<213> Homo sapiens

<400> 578

```

Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu Leu Tyr Ile Arg His
              5              10              15
His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr Lys Lys Leu Asn Tyr
              20              25              30
Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His Ile Ala Lys Val Tyr
              35              40              45
Gln Pro His
50

```

<210> 579

<211> 56

<212> PRT

<213> Homo sapiens

<400> 579

```

Met His Phe Thr Phe Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu
              5              10              15
Leu Tyr Ile Arg His His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr
              20              25              30
Lys Lys Leu Asn Tyr Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His
              35              40              45
Ile Ala Lys Val Tyr Gln Pro His

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206

50

55

<210> 580
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 580
 Met Glu Leu Arg Thr Lys Ala Leu Arg Thr Ala Gln Gln Leu Thr Ser
 5 10 15
 Cys Val Thr Ala Leu Lys Ala Ala Gly Pro Pro Leu Thr Phe Trp Lys
 20 25 30
 Gly Lys Trp Val Gln Cys Cys Leu Pro Leu Trp Gly Leu Leu Gly Ser
 35 40 45
 His Ala Phe Tyr Ile Tyr Ala Val Asp Ile Phe Met Phe Pro Gly Ser
 50 55 60
 Phe Ile His
 65

<210> 581
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 581
 Met Leu Glu Val Lys Phe Glu Val Ser Leu Arg Pro Thr Gly Asn Glu
 5 10 15
 Thr Ala Gly Gln Thr His Gly Thr Gln Asp Lys Gly Ser Lys Asp Ser
 20 25 30
 Thr Ala Ala Asp Ile Leu Cys Asp Ser Leu Glu Ser Ser Arg Pro Ala
 35 40 45
 Ala His Ile Leu Glu Gly Lys Met Gly Thr Met Leu Ser Ala Thr Leu
 50 55 60
 Gly Pro Ser Trp Val Thr Cys Ile Leu His Leu Cys Ser
 65 70 75

<210> 582
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 582
 Met Leu Phe Leu Gln Thr Ile Asp Thr Lys Cys Thr Gly Ile Glu Ile
 5 10 15
 Asn Arg Asn Trp Ser Lys Val Trp His Thr His Ser His Val Asp Val
 20 25 30
 Lys Leu Cys Leu Glu Phe Leu Cys Gly Val Trp Phe Gly Leu Gly Phe
 35 40 45
 Leu Gly Val
 50

<210> 583
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 583
 Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg

207

```

          5          10          15
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
          20          25          30
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
          35          40          45
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
          50          55          60

```

<210> 584

<211> 76

<212> PRT

<213> Homo sapiens

<400> 584

```

Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
          5          10          15
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
          20          25          30
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
          35          40          45
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
          50          55          60
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
          65          70          75

```

<210> 585

<211> 50

<212> PRT

<213> Homo sapiens

<400> 585

```

Met Val Tyr Arg Phe Gly Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu
          5          10          15
Ala Ser Leu Gly Ser Ser Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp
          20          25          30
Arg Gln Ala Asp Pro Ser Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu
          35          40          45
Leu Phe
          50

```

<210> 586

<211> 60

<212> PRT

<213> Homo sapiens

<400> 586

```

Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
          5          10          15
Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
          20          25          30
Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
          35          40          45
Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
          50          55          60

```

<210> 587

<211> 1408

<212> DNA

<213> Homo sapiens

<400> 587

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cggtcctgta cgatttcagt atgtcttaac cgcagctgtg attggaacaa ttcagattgc 960
tgtcatctgt gtggtgggtcc tctgcatcac aaggaaatgc ccagaagca acagaattca 1020
cagacagaag caaaatacag ggcactacag ttcagacaat acaacaagag cgtccacgag 1080
gttaattctaa agggagcatg tttcacagtg gctggactac cgagagcttg gactacacaa 1140
tacagtatta tagacaaaag aataagacaa gagatctaca catgttgctt tgcatttgtg 1200
gtaatctaca ccaatgaaaa catgtactac agctatatatt gattatgtat ggatatattt 1260
gaaatagtat acattgtctt gatgtttttt ctgtaatgta aataaactat ttatatcaca 1320
caatawagtt ttttctttcc catgtatttg ttatatataa taaatactca gtgatgagaa 1380
aaaaaaaaa aaaaaaaaaa rwmgaccc 1408

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<210> 588

<211> 81

<212> PRT

<213> Homo sapiens

<400> 588

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Met Pro Gln Lys Gln Gln Asn Ser Gln Thr Glu Ala Lys Tyr Arg Ala
                    5                      10                      15
Leu Gln Phe Arg Gln Tyr Asn Lys Ser Val His Glu Val Asn Leu Lys
                    20                      25                      30
Gly Ala Cys Phe Thr Val Ala Gly Leu Pro Arg Ala Trp Thr Thr Gln
                    35                      40                      45
Tyr Ser Ile Ile Asp Lys Arg Ile Arg Gln Glu Ile Tyr Thr Cys Cys
                    50                      55                      60
Leu Ala Phe Val Val Ile Tyr Thr Asn Glu Asn Met Tyr Tyr Ser Tyr
                    65                      70                      75                      80
Ile

```

<210> 589

<211> 157

<212> PRT

<213> Homo sapiens

<400> 589

```

Met Thr Met Cys Leu Cys Val Ala Pro Met Gly Arg Ala Thr Arg Met
                    5                      10                      15
Ser Val Thr Cys Asp Arg Leu His Ala Asn Ser Arg Val Arg Tyr Leu
                    20                      25                      30
Trp Cys Gln Lys Asp His Val Pro Gln Met Gln Asp Gln Asp Leu Glu

```

209

```

      35      40      45
Met Glu Ser Met Lys Ala Leu Glu Lys Leu Val Lys Arg Arg His Pro
  50      55      60
Pro Val Ile Phe Ala Ser Leu Val Gln Asn Val Thr Lys Met Pro Arg
  65      70      75      80
Met Ser Gly Val Cys Val Ile Leu Thr Val Leu Lys Pro Thr Ser Ile
      85      90      95
Pro Ser Ala Leu Met Gly Asn Leu Met Ile Met His Ala Lys Ser
      100      105      110
Lys Lys His Arg Val Arg Asn Arg Arg Lys Leu Lys Ser Cys Leu Trp
      115      120      125
Val Asp Val Lys Ile Thr Gln Leu Gln Leu Leu Ser Leu Lys Met Gly
      130      135      140
Ile Met Gln Glu Gln Ile Met Gln Arg Met Leu Thr Asn
145      150      155

```

<210> 590
 <211> 347
 <212> PRT
 <213> Homo sapiens

```

<400> 590
Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe Pro Thr
      5      10      15
Ser Leu Ser Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr
      20      25      30
Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys Lys
      35      40      45
Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys Val Cys
      50      55      60
Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly
      65      70      75      80
Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln
      85      90      95
Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr Asp Ala
      100      105      110
Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu Thr Ser
      115      120      125
Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu Cys
      130      135      140
Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp Cys Ser
145      150      155      160
Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr Asp
      165      170      175
Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys Ile
      180      185      190
Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr Thr
      195      200      205
Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn Ala
      210      215      220
Asn Lys Leu Glu Glu Ser Ala Arg Glu His His Ile Pro Cys Pro Glu
225      230      235      240
His Tyr Asn Gly Phe Cys Met His Gly Lys Cys Glu His Ser Ile Asn
      245      250      255
Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His
      260      265      270
Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val

```

210

275 280 285
 Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile
 290 295 300
 Ala Val Ile Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg
 305 310 315 320
 Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser
 325 330 335
 Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
 340 345

<210> 591
 <211> 565
 <212> DNA
 <213> Homo sapien

<400> 591
 actaaagcaa atgaacaagc tgacttgcta gtatcatctg cattcattga agcacaagaa 60
 cttcatgcct tgactcatgt aaatgcaata ggattaaaaa ataaatttga tatcacatgg 120
 aaacagacaa aaaatattgt acaacattgc acccagtgtc agattctaca cctggccact 180
 caggaagcaa gagttaatcc cagaggtcta tgtcctaattg tgttatggca aatggatgtc 240
 atgcacgtac cttcatttgg aaaattgtca tttgtccatg tgacagttga tacttattca 300
 catttcatat gggcaacctg ccagacagga gaaagtactt cccatgttaa aagacattta 360
 ttatcttgtt ttcctgtcat gggagttcca gaaaaagtta aaacagacaa tgggccagggt 420
 tactgtagta aagcatttca aaaattctta aatcagtggg aaattacaca tacaatagga 480
 attctctata attcccaagg acaggccata attgaaggaa ctaatagaac actcaaagct 540
 caattgggta aacaaaaaaa aaaaa 565

<210> 592
 <211> 188
 <212> PRT
 <213> Homo sapien

<400> 592
 Thr Lys Ala Asn Glu Gln Ala Asp Leu Leu Val Ser Ser Ala Phe Ile
 1 5 10 15
 Glu Ala Gln Glu Leu His Ala Leu Thr His Val Asn Ala Ile Gly Leu
 20 25 30
 Lys Asn Lys Phe Asp Ile Thr Trp Lys Gln Thr Lys Asn Ile Val Gln
 35 40 45
 His Cys Thr Gln Cys Gln Ile Leu His Leu Ala Thr Gln Glu Ala Arg
 50 55 60
 Val Asn Pro Arg Gly Leu Cys Pro Asn Val Leu Trp Gln Met Asp Val
 65 70 75 80
 Met His Val Pro Ser Phe Gly Lys Leu Ser Phe Val His Val Thr Val
 85 90 95
 Asp Thr Tyr Ser His Phe Ile Trp Ala Thr Cys Gln Thr Gly Glu Ser
 100 105 110
 Thr Ser His Val Lys Arg His Leu Leu Ser Cys Phe Pro Val Met Gly
 115 120 125
 Val Pro Glu Lys Val Lys Thr Asp Asn Gly Pro Gly Tyr Cys Ser Lys
 130 135 140
 Ala Phe Gln Lys Phe Leu Asn Gln Trp Lys Ile Thr His Thr Ile Gly
 145 150 155 160
 Ile Leu Tyr Asn Ser Gln Gly Gln Ala Ile Ile Glu Gly Thr Asn Arg
 165 170 175
 Thr Leu Lys Ala Gln Leu Val Lys Gln Lys Lys Lys
 180 185

211

<210> 593
 <211> 271
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(271)
 <223> n = A,T,C or G

<400> 593
 actttatggt cnagtgcana aancncctg gattgccacc ntactctcag ggctgtgant 60
 tgtgcnecca nagcaacctg ggcaacgagg gacagggggg ccnacaattg agggagcggt 120
 gtccctagct ggggtctata catgncnggg naagggcngc tgagtnccat nagcaaagga 180
 nctagnatnt gcgggggtgc ggccctgggccc taccctttta agcatccntn gatccactcc 240
 angaancng gggtagnacg gtttnccaac a 271

<210> 594
 <211> 376
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(376)
 <223> n = A,T,C or G

<400> 594
 cctttggggg nggggggaac ctttaccatt gtnccctttt atttcatttg gttnggggttc 60
 gcgccctcnn gggccaacaa agttatcgtn nttgaagaga anattttttt ggnttngncc 120
 cgattaagcg ncaaagtgtg agcaaaaangc cgtgccactt gtggcgtagc tncgtcgggt 180
 cgattcgacg acaaggcgtn gcgcgntanc gttagtctcn aatngaccn gtggcatgag 240
 cccacgangg nttcgtgtcg tcacatggnc tctagacata acgcncnccn ttttttncag 300
 agggggntgc cgcccttagg gaggnagggg tggggacact agccaancca nantctnacc 360
 ccattgaaga aaaggn 376

<210> 595
 <211> 242
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(242)
 <223> n = A,T,C or G

<400> 595
 agnctgctgn tcgtnccctn tatgtggctt catnntgagg acaanagtng cactgaggct 60
 tgnqnatgcc aggcaaggnc aagctggctc aaaaagcatc caccacctc tgnaanggggt 120
 atgccangag cangtgcacc agtcccaact angagnccn ggcatgntac atcttcttcc 180
 acccctnaaa ntttngncta caangnccat tttttttttt ctcttaaggg ncncttggtc 240
 tc 242

<210> 596
 <211> 535
 <212> DNA
 <213> Homo sapien

212

<220>

<221> misc_feature

<222> (1)...(535)

<223> n = A,T,C or G

<400> 596

accagttgga	tactgctaaa	nagatattta	tgcagcctca	tatgttaagt	cgtatatattt	60
gaaagctttt	taaatTTTTT	ctttaagaag	atttttagatg	cttatcactg	agtaccagag	120
ggatgtaggc	tgatgccctt	atcaacaaag	tcagggactg	tggcacacaa	ggattgacta	180
ctgcagacac	ggccacaatg	ctacctctag	agggcctgaa	tccccctgcc	ctctctggtg	240
gggagaaggg	ctggcagagc	cattagcatg	ggctccggcc	aatcctggcc	actttgacac	300
tcctggtgct	gacccagggt	cctggaggaa	gggatgaggt	gggcagtaga	gatgtcagg	360
gcagtggccc	ctttccatcc	acactggaac	tatttcagta	ttttaccacc	aattcagcca	420
ttcccttggt	cgctggctga	acatcagccc	tgctccaggt	ctcagtttcc	cctttgtaaa	480
gggaaagctc	tggattcagg	gagtgatgaa	gaggtcatca	tgggtcttgag	aattc	535

<210> 597

<211> 257

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(257)

<223> n = A,T,C or G

<400> 597

tttchnatacc	caaaantacc	ccatattang	accanacatt	tgtctnngaa	aaattaccat	60
tntntaacnt	ttggggccacc	tgagannaaa	tggtgtgaat	ncatgataag	atggancagn	120
attnctctta	agatnngatn	agaccccggt	tttcacggaa	catatccaag	nacccaatag	180
gnaacaagcc	acgggngggag	tcacaaacat	atattcttta	ctctcataat	ccgtnncaca	240
naactnttgn	acttgac					257

<210> 598

<211> 222

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(222)

<223> n = A,T,C or G

<400> 598

nntggntacc	gtcnaaactt	nncttggtac	ccgagctcgg	atccactagt	ccagtgtggt	60
ggaattccat	tgtgttgggc	tataagctgt	aatagtggag	ncgtgctngg	ttcattgcan	120
nagnccctcc	gcanncacnc	ttgmnaaac	ctgtgagnag	gcnataaatt	attcacataa	180
tcactactgc	atgaanctga	ctcaaacyca	tccacntaca	cc		222

<210> 599

<211> 238

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(238)

213

<223> n = A,T,C or G

<400> 599

gcatgacatc	ancgatgtnt	ttggnnacct	ganattngct	aaaactngng	natgccgggn	60
atgnagggtt	ggtantgatc	tatgcactca	catctcatgg	ggacgtttca	tgtggagtgn	120
tcgacaangt	tgctgnancn	gagaagtgat	gatctcagtt	gaaaggggtca	tgtgaataca	180
cnttacactt	gaaaaagaag	cacattggga	atatcacgaa	acgnccacca	acatcctg	238

<210> 600

<211> 232

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(232)

<223> n = A,T,C or G

<400> 600

cgaactat	agactaccta	ggaaaattat	tttagtatca	gaagaatata	aggggtgtag	60
tactcatcag	agctaaatga	gagcgcttta	aaaatgttag	tttgtcttcc	gccatttcta	120
cagaaagctg	caatttcagg	ttttcaacct	aataggtgat	atttaanaaa	aaaaaaaagc	180
aatcgcaaat	agccccactg	cttttacaaa	tcattttttc	cccaacacaa	tg	232

<210> 601

<211> 547

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(547)

<223> n = A,T,C or G

<400> 601

cattgtgttg	gggaaaaaat	gatttgtata	agcagtgggg	ctatttgcca	ttgctttttt	60
tttttcttaa	atatcaccta	ttagggtgaa	aacctgaaat	tgcagctttc	tgtagaaatg	120
gcggaagaca	aactaacatt	tttaaagcgc	tctcatttag	ctctgatgag	tactacaccc	180
ctnatattct	tctgatacta	aaataatttt	cctagtgtag	tctaaacttt	tttaaaaaga	240
catgtaatcc	gcggagttag	taactcaaaa	cgagtgcata	tnnggaagtat	cgcagccggt	300
nctggatnaa	attcccagct	tgctngcttg	ctnagccggg	gggaggtnaa	aaaaacatct	360
gcagcccnng	ggnaaaaacc	ttcgatttgt	tcttacgtgt	ttacgttatt	ttatttccct	420
nnagcaaggc	nggganttgg	ggactcgaaa	tggtacagtt	gggctgggga	tcgcccttgt	480
tacataaaag	ncgtccagaa	gagggacggt	tacaggcnng	ganctccaaa	ggtcagtcct	540
tgccatt						547

<210> 602

<211> 826

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(826)

<223> n = A,T,C or G

<400> 602

cgggggggnt	tacgtctctc	tggacgcttt	tattgtacca	gggcgatccc	agcccaactg	60
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214

taccattcga	gtccctactc	ctgccttgct	ctagggaat	aaaataacgt	aaacacgtaa	120
gaacaatgcy	aaagcgtttt	cttccttagg	ctgcagattg	tcttcttcac	cgccctgct	180
tagctagcta	gctagctggg	aatttaatcc	agaaacggct	tgcgatacct	cctagatgca	240
ctcgttttga	gttacaaact	ccgcggatta	catgtctttt	taaaaaagtt	tagactacac	300
tagggaaaat	tatttttagta	tcagaagaat	atcagggggt	gtagtactca	tcagagctna	360
atgagagcgc	tttaaaaaatg	ttagtttgct	ttccgccatt	tctacagaaa	gctgcaattt	420
caggttttca	ncctaataag	tgatatntaa	gaaaaaaaaa	acaatcgcan	atagccact	480
gcttttacaa	atcatttttc	tcttctaggt	atagcctgtc	aggtggccta	atgtattttt	540
gacatctcta	ggaattttta	tagaccagaa	atgggtgccca	gagatatgcc	tgactaatc	600
tttaagtggg	atztatgtat	ttctcaanca	agtgattaaa	gcaaaactag	gcacgaatga	660
aatcaagatc	tttaggccag	aaatcatgaa	nanttttana	attattttan	gaatctgtgg	720
cttctcttct	taaaatngaa	aaaaaaattg	tttaaaccce	naaggctctga	ataccceagc	780
ncctgaacn	anagaacaan	gccggagcac	cccctcccaa	atcccc		826

<210> 603

<211> 817

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(817)

<223> n = A,T,C or G

<400> 603

nnangacttt	tgtggtntta	tacaattntt	ttttctattt	ctatgaagag	aaagccacag	60
agtcctaaaa	taattctaaa	actcatcatg	actttcttgc	ctaaaagatc	ttgatttcaa	120
tcgtgcctag	ttttgcttta	atcacttgct	tgagaaatac	ataaatcccc	acttaagatt	180
agtgcaggca	tatctctggc	acccatttct	ggttctatta	aaattcctag	agatgtcaaa	240
aattacatta	ggccacctga	caggctatac	ctagaagaga	aaaaatgatt	tgtaaaagca	300
gtggggctat	ttgcgattgc	tttttttttt	tcttaaatat	cacctattag	gttgaaaacc	360
tgaaattgca	gctttctgta	gaaatggcgg	aagacaaact	aacattttta	aagcgctctc	420
atthagctct	gatgagtact	acacccctga	tattcttctg	atactaaaat	aattttccta	480
gtgtagtcta	aactttttta	aaaagacatg	taatccgcgg	agtttgtaac	tcaaaacgag	540
tgcatctagg	aggtatcgca	agccgtttct	ggattaaatt	cccagctagc	ttgcttgctt	600
agcaggggcy	ggnaaanaag	acatctgcag	cctagggaag	aaaacccttc	gcattgttct	660
tacgtgttta	cgttatttta	tttccctanaa	caaggcngaa	ttggggactcg	aatggttcag	720
ttgggggtgg	ggatccctcg	gtncataaaa	ngtcanaaag	anggtacag	cggaaaccca	780
agggctcgcc	tgcatttana	ctcggaattt	tggtgccc			817

<210> 604

<211> 694

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(694)

<223> n = A,T,C or G

<400> 604

cttttcaaat	catttttntct	cttctaggta	tancctgtca	ggtggcctaa	tgtaattttt	60
gacatctcta	ngaattttta	tagaaccaga	aatgggtgcc	agagatatgc	ctgcactaat	120
cttaagtggg	gatttatgta	tttctcaagc	aagtgtataa	agcaaaacta	ggcacgattg	180
aatcaagat	cttttaggca	anaaagtcac	gatgagtttt	agaattattt	taggactctg	240
tggttttctc	ttcatagaaa	tagaaaaaaa	aattgtataa	aaccacaaaa	ggtcctgaat	300
agccaaagca	acactganca	aaaagaacan	agcaggaag	caacacacta	ccngaattca	360
aattatacta	ccagggtgta	gtaacaaaaa	cagcattcta	ttggcataaa	atagacacca	420

215

agaccaatgg	ancagaataa	agaacccccac	aaataaatcc	atatatntac	cgccanctga	480
ttatcaataa	cnaacaccaa	gaacatatnt	taagggaant	nctattcaat	aantagtgct	540
ggnaaaaact	gggaaatcca	tatgcagaaa	naatgaaact	agacccttat	ccctcaccat	600
acgcaaannt	caacttcgga	atgggattac	aaaacttaag	acattccaac	ccaagaaact	660
atnaaancta	ctattaagaa	aacagatcnc	nccc			694

<210> 605
 <211> 678
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (678)
 <223> n = A,T,C or G

<400> 605						
taaaaatcta	gactacacta	ggaaattatt	ttantatcag	aagaatatca	ggggtgtagt	60
actcatcana	gctaaatgag	agcgctttaa	aaatggttagt	ttgtcttccg	ccatttctac	120
agaaagctgc	aatttcagggt	tttcaaccta	atagggtgata	tttaagaaaa	aaaaaaagca	180
atcgcaaata	gccccactgc	ttttacaaat	catttttttct	cttctaggta	tagcctgtca	240
ggtggcctaa	tgtaattttt	gacatctcta	ggaattttta	tagaaccaga	aatgggtgcc	300
agagatatgc	ctgcactaat	cttaagtggg	gatttatgta	tttctcaagc	aagtgattaa	360
agcaaaaacta	ggcacgattg	aaatcaanat	cttttaggca	agaaagtcac	gatgagtttt	420
anaattatttt	taggactctg	tggctttctc	ttcatagaaa	tagaaaaaaa	aaattgtata	480
aaaaccacaa	aaggtcctga	atagcccaaa	gcaacactga	acaaaangaa	caaagcagga	540
agcaacacac	taccggaatt	caattatact	accaaggtgt	antaaccaa	acagcattct	600
attgggcata	aaatagacca	aagaccagtg	ggaaacagaa	taaagaancc	caaaataaat	660
cctatatatta	cngccnc					678

<210> 606
 <211> 263
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (263)
 <223> n = A,T,C or G

<400> 606						
gtggggtcng	cancagccaa	ctcagcttcc	tttcgggctt	tgttagcaga	cggatcatcc	60
tctagtccac	tgtgntcaaa	ttccattgtg	tgggggccnc	tcgcctcggc	canagatctg	120
agtgancana	cntgtcccca	ctgaggtgcc	ccacagcngn	ttgtnttcag	cangggctna	180
caactcgacc	ggcagcgnan	ggctggcaga	antgngcgcc	tnnctcattc	ctacgcngtn	240
ngccgcagga	aggangacag	gcc				263

<210> 607
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 607		
ccatgtgggt	cccggttgtc	tt
		22

216

<210> 608
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 608
gätaggggtg ctcaggggtt gg

22

<210> 609
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 609
gctggacagg gggcaaaagc tggggcagtg aaccatgtgc

40

<210> 610
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 610
ccttggtccag atagcccagt agctgac

27

<210> 611
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 611
gatagagaaa accgtccagg ccagtattgt gggaggctgg gagtgc

46

<210> 612
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 612
gcacatgggt cactgcccc gcttttgccc cctgtccagc

40

<210> 613
<211> 38
<212> DNA

217

<213> Artificial Sequence

<220>

<223> Primer

<400> 613

gccgctcgag ttagaattcg gggttggcca cgatgggtg

38

<210> 614

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 614

ggcggggcat atgcatcacc atcaccatca catcataaac ggcgaggact gca

53

<210> 615

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 615

gcactcccag cctccacaa tactggcctg gacggttttc tctatc

46

<210> 616

<211> 1350

<212> DNA

<213> Homo sapien

<400> 616

atgcatcacc	atcaccatca	catcataaac	ggcgaggact	gcagcccgca	ctcgcagccc	60
tggcaggcgg	cactggtcat	ggaaaacgaa	ttgttctgct	cgggcgtcct	ggtgcatccg	120
cagtgggtgc	tgtcagccgc	acactgtttc	cagaactcct	acaccatcgg	gctgggcctg	180
cacagtcttg	aggccgacca	agagccaggg	agccagatgg	tggaggccag	cctctccgta	240
cggcaccag	agtacaacag	acccttgctc	gctaacgacc	tcatgctcat	caagttggac	300
gaatccgtgt	ccgagctgta	caccatccgg	agcatcagca	ttgcttcgca	gtgccctacc	360
gcggggaact	cttgccctcgt	ttctggctgg	ggtctgctgg	cgaacggcag	aatgcctacc	420
gtgctgcagt	gcgtgaacgt	gtcgggtggtg	tctgaggagg	tctgcagtaa	gctctatgac	480
ccgctgtacc	acccagcat	gttctgcgcc	ggcggagggc	aagaccagaa	ggactcctgc	540
aacggtgact	ctggggggcc	cctgatctgc	aacgggtact	tgcagggcct	tgtgtctttc	600
ggaaaagccc	cgtgtggcca	agttggcgtg	ccagggtgtc	acaccaacct	ctgcaaattc	660
actgagtgg	tagagaaaac	cgtccaggcc	agtattgtgg	gaggctggga	gtgcgagaag	720
cattcccaac	cctggcaggt	gcttgtggcc	tctcgtggca	gggcagtctg	cggcgggtgt	780
ctggtgcacc	cccagtggtg	cctcacagct	gccactgca	tcaggaacaa	aagcgtgac	840
ttgctgggtc	ggcacagcct	gtttcatcct	gaagacacag	gccaggtatt	tcaggtcagc	900
cacagcttcc	cacacccgct	ctacgatatg	agcctcctga	agaatcgatt	cctcaggcca	960
ggtgatgact	ccagccacga	cctcatgctg	ctccgcctgt	cagagcctgc	cgagctcacg	1020
gatgctgtga	aggtcatgga	cctgcccacc	caggagccag	cactggggac	cacctgctac	1080
gcctcaggct	ggggcagcat	tgaaccagag	gagttcttga	ccccaaagaa	acttcagtgt	1140
gtggacctcc	atgttatttc	caatgacgtg	tgtgcgcaag	ttcacctca	gaaggtgacc	1200
aagttcatgc	tgtgtgctgg	acgctggaca	gggggcaaaa	gctggggcag	tgaaccatgt	1260
gccttgcccg	aaaggccttc	cctgtacacc	aaggtggtgc	attaccggaa	gtggatcaag	1320

218

gacaccatcg tggccaaccc cgaattctaa

1350

<210> 617

<211> 449

<212> PRT

<213> Homo sapien

<400> 617

Met	His	His	His	His	His	His	Ile	Ile	Asn	Gly	Glu	Asp	Cys	Ser	Pro	1	5	10	15
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Val	Met	Glu	Asn	Glu	Leu	Phe	20	25	30	35
Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val	Leu	Ser	Ala	Ala	His	40	45	50	55
Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu	Gly	Leu	His	Ser	Leu	Glu	60	65	70	75
Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val	Glu	Ala	Ser	Leu	Ser	Val	80	85	90	95
Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	100	105	110	115
Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	120	125	130	135
Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	140	145	150	155
Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	160	165	170	175
Val	Asn	Val	Ser	Val	Val	Ser	Glu	Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	180	185	190	195
Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly	Gly	Gly	Gln	Asp	Gln	200	205	210	215
Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	220	225	230	235
Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	240	245	250	255
Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	260	265	270	275
Glu	Lys	Thr	Val	Gln	Ala	Ser	Ile	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	280	285	290	295
His	Ser	Gln	Pro	Trp	Gln	Val	Leu	Val	Ala	Ser	Arg	Gly	Arg	Ala	Val	300	305	310	315
Cys	Gly	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val	Leu	Thr	Ala	Ala	His	320	325	330	335
Cys	Ile	Arg	Asn	Lys	Ser	Val	Ile	Leu	Leu	Gly	Arg	His	Ser	Leu	Phe	340	345	350	355
His	Pro	Glu	Asp	Thr	Gly	Gln	Val	Phe	Gln	Val	Ser	His	Ser	Phe	Pro	360	365	370	375
His	Pro	Leu	Tyr	Asp	Met	Ser	Leu	Leu	Lys	Asn	Arg	Phe	Leu	Arg	Pro	380	385	390	395
Gly	Asp	Asp	Ser	Ser	His	Asp	Leu	Met	Leu	Leu	Arg	Leu	Ser	Glu	Pro	400			
Ala	Glu	Leu	Thr	Asp	Ala	Val	Lys	Val	Met	Asp	Leu	Pro	Thr	Gln	Glu				
Pro	Ala	Leu	Gly	Thr	Thr	Cys	Tyr	Ala	Ser	Gly	Trp	Gly	Ser	Ile	Glu				
Pro	Glu	Glu	Phe	Leu	Thr	Pro	Lys	Lys	Leu	Gln	Cys	Val	Asp	Leu	His				
Val	Ile	Ser	Asn	Asp	Val	Cys	Ala	Gln	Val	His	Pro	Gln	Lys	Val	Thr				

219

Lys Phe Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Trp Gly
 405 410 415
 Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val
 420 425 430
 Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro Glu
 435 440 445
 Phe

<210> 618
 <211> 385
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(385)
 <223> n = A,T,C or G

<400> 618
 ctgtgctgag aacccaaaagc tatgancact gcttttccaa atgtccataa naccaacatt 60
 tttatcacta ccaccatcac ctgggagctc nttagaaagc tagtctcccg ggcaccaccc 120
 tggcctactg aacctaattgt gcattttaaca agattnacgt ngaaatctgc aaagcacagg 180
 ggcngataac agtaccacct gntctgggtc ctanccccan gacccttaca gtctaactgg 240
 gacacaaggg cttnaaatca aattgcctat cattaagata tacaanganc ntgagaaact 300
 gctncactta tntattaagg ngctctaaga cttagaaacn aaangcantg ctgagangat 360
 tcaaatatga ngggggncac tttnc 385

<210> 619
 <211> 869
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(869)
 <223> n = A,T,C or G

<400> 619
 gatatcccgg gaattcgcgg ccgcgtcgac ctctacttgt ttagacataa atgcagtcta 60
 gcattaaaga tccttttaaaa aaatgttttc ccaatgggta aaagacaagc tcaaataaat 120
 gaactctcat acatatgcca aaattgatga gtagataaat atttcagtag gtagttacta 180
 gctttctgtg tatgagtaaa catatgggag aaattttaaaa cactaaagta gactcaatga 240
 aagcatagta tcctatgtat tcgtttttca gaaatgtcta atgaagggaag gaaacaatga 300
 atgaatgccc ttattcctct tagagtgtcg ggacatgggt ttgcctgaaa acttcatgtg 360
 aattttatat tttgctacac attacaccca tcttagactt atacgtataa gacataaggc 420
 atatcttatg tcttacatgt ataataatct aagcagaaca aaaaataacg aaatattttc 480
 ttccccaat ttttgagaca gatggatttt ccggaaagat gtgttttagct tttaatcctg 540
 tgggttttgtg taccacctgg cacactagag tgttgctcta attcagttag ttgtaactct 600
 ggggtgaacag tggaaatact aggggtacatt ttaaaaatgc taatgctcgg gcctcgtga 660
 agaccaaatt aattggaatc tctgngggng gnattgatct ttttataatc tttctanang 720
 attctaattg gcttccagg atgaaaacn ctgntggagc tnggaacctt cctttagttt 780
 ggagaaaccc cgatgagggt ntnttaggcn ccgcctnttt ttggcctggg cttccccct 840
 tatntnttt tggaangnc cnaattttt 869

<210> 620
 <211> 339
 <212> DNA

220

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(339)

<223> n = A,T,C or G

<400> 620

gngcgggcct	cnccggtgctt	gctctcgctg	ccgacgctct	ttttccacca	gctgtaggan	60
aagcccgaag	accactggtc	ccccgggtag	cccaagtacc	actgggtcctc	ctgggtcctg	120
acgctncggg	tcttctcgt	ggcgtagact	gccagcttcg	gagaccctc	agcccctccc	180
cgcttttctc	caccccagga	ggccatcagt	agcgagctac	tgctctgggc	acaacctccc	240
agcangatag	cccgcggttt	ccaatctgcg	aaaggaggac	cgccnagccc	gaaatgccna	300
gcccagcnat	cactgccacg	ccgagccnag	cgtctgtgc			339

<210> 621

<211> 267

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(267)

<223> n = A,T,C or G

<400> 621

gggngcatg	gtccnngta	gccaagtaca	tggtcctcct	ggctcctgac	gctacgggtc	60
ttcctegtgg	cgtagactgc	cagcttcgga	gacccctcag	ccctccccc	ctttctcca	120
ccccaggagg	ccatcagtag	cgagctactg	cctcgccac	aacctccag	caggatngcc	180
cgcggtttcc	aatctgcgaa	aggaggaccg	cnagccaga	aatgccnagc	cnagcgatca	240
ctgccacgcc	nagccnagcg	ctcgtgc				267

<210> 622

<211> 847

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(847)

<223> n = A,T,C or G

<400> 622

cttangntgt	cgactgacgt	catgcatgan	ttaaagcaga	ggtttggtga	aatttatgaa	60
aaatacaaaa	ttccggcttg	tcctgaggaa	gagccactac	ttgataactc	tacaagagga	120
acagatgtga	aggatattcc	ctttaatttg	acaaataaca	tacctgggtg	tgaggaagaa	180
gatgcatctg	aaatatctgt	ctcagtggta	ttcgagacat	ttcctgaaca	aaaagaaccc	240
agtctcaaaa	atatcatcca	tccatactat	catccgtact	ctgggtccca	ggaacatgtt	300
tgccagtcac	cttctaagct	tcattttacat	gaaaataaat	tagactgcga	caatgataac	360
aaactaggca	ttggacatat	ttttagtaca	gataacaact	ttcataatga	tgcaagcact	420
aagaaagcaa	ggaacccaga	agtggttacg	gttgaaatga	aagaagacca	agagtttgat	480
ttgcaaatga	caaaaaatat	gaacccaaat	agtgacagtg	gcagtacaaa	taactataaa	540
agcctgaaac	ctaaattaga	aaatctgagt	tctttaccac	cagattctga	cagaacatca	600
ggaagtatat	ctacatgaag	aattacagca	agacatgcc	aaagtttaag	aatgangtca	660
acacattaga	aanaagantt	ctgggctttg	aagaaagaaa	atgttccact	tcataaagaa	720
ggttgaaaga	agaatgggag	agcccngaan	tttttgcccn	gaaattttcg	ggaaccctac	780
tggtatgggc	nactggttgg	ccatgaatga	ataatggact	aatcnnccaa	ttcctngggg	840
agggaat						847

221

<210> 623
 <211> 681
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(681)
 <223> n = A,T,C or G

<400> 623
 aaaactgtac tcgcgcgctg catgtcgaca ctagtggatc caaagaatcg gcacgagcga 60
 aaangctcan gcagcccggc tggccgcgcg cgctcctccc ccaggaaag ccaangtgga 120
 ngctgatgtg gctgcangag ctogtttcac agcccctcan gtgganctgg ttgggccgcg 180
 gctgccangg gcggaagtgg gtgtccccc cangtcagccc caaggctgcc cctcaciaaag 240
 cactgggtgt ttgcctccac tgccaccttg ggctccgaac ccgctcccct gctgtggang 300
 cccaccgtgg gaatccagggt ccccagggtg actgcctgcc ttgccctcac tgccactct 360
 gcccacactt ccctgcctag anaccgggaa ggggtgtgt cggtantggt gcccacttg 420
 atgtggcagc accgactgtg ggggtggacc tggccttgcc ggggtgcaaaa gtggggggccc 480
 ngggaaaagc acctgaagtg gccctgaaaa atccccctt aatttttccc caatttgggg 540
 ctcaacaaa aggaaattgc tgaagccaan ggtaccaagg tcaaccctaa ggccagggtg 600
 aaaaggtccc aaaattccaa tccccacctt ttgggcttnc ctcttggaac cccggccccc 660
 tctcntgaan ttttaaaaaa n 681

<210> 624
 <211> 661
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(661)
 <223> n = A,T,C or G

<400> 624
 attggtctta ctgtaccacc ggggtggaat cgatggccgc ggcgtctaaa tatccgattt 60
 tttttttttt tctctttctg actgtccatg gacaaatgaa actaacttaa tctaactaaa 120
 aaacacaact atattttgaa gattttctat ctgcactcaa ggacactttc cacnccgttg 180
 ttgttacctt ttgggtcttg ctctgaacat gaaattnatc tcaagggatt ngatttctgg 240
 acctcctatt cctgctatgg gtttgatatt tcttgggctc cagggccact gttgcattgg 300
 gntgacagnt acctcctagc ccatancctc ctatcttggg aaacaaacct aacaactacg 360
 tgtaccttcc atagatctct gattgagtct cagtatnccg ttgctcatgg gcgattcact 420
 tgaatccgtn attgggtgcca acaatcctga ctcatggggn aatggatcct atcacgttcc 480
 cctgattngc aaccctgta tacatanatc taatcgcata gaatctagcn tnggntatgc 540
 gcggctacgc tatcagggnt tgntaactat ngcatggcta cgaancctga tcatgatcna 600
 ggggtcatgga ctcttatcag ggggggttgg ccngcttct ttttcnnacc ttggtaaaac 660
 c 661

<210> 625
 <211> 181
 <212> DNA
 <213> Homo sapien

<400> 625
 gcaacaatca gatcatgta aagtaaatct ccattgccct ggatcacttc aggatttaat 60
 tgtccaagga gagcagggtt ctctgtgaa aaaaagggtg ggaaatgttt gagagtaaaa 120
 aatacaaaat tcaaccgggtc gaaaatacac cactccattc agtgctctac ccccataaagc 180

222

c 181

<210> 626
 <211> 181
 <212> DNA
 <213> Homo sapien

<400> 626
 gcaacaatca gatcatgtta aagtaaattct ccattgccct ggatcacttc aggatttaaat 60
 tgtccaagga gagcagggtt ctctgtgaa aaaaagggtg ggaaatgttt gagagtaaaa 120
 aatacaaaat tcaaccggtc gaaaatacac cactccattc agtgctctac ccccataagc 180
 c 181

<210> 627
 <211> 813
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(813)
 <223> n = A,T,C or G

<400> 627
 accaagctgg agctcgcgcg cctgcaggtc gacactagtg gatccaaagt gaacgtgaag 60
 gtgagcagag gagaacttgc gatggcaaag ttaaaaacaa gaggagatga tggctcttgg 120
 gtggcacagg atgttaaaaa aattctcctg tccttaagga gttactgcta tttgagtaat 180
 gtgccacttc cctacatagc cttctatgca gaaatgctat atttccactt cacaaccag 240
 aacgtgcatt ttattttaca tttagaggag gaacaaacaa ccagaaggca aaaactggtg 300
 cattatTTTT tgcaattctc ttggaaagag ttcgttttta acttctgctc agacagcaca 360
 caactactgg gaatatattt taatttcaaa tctgatgtgt gacatctggg aactcattta 420
 ttgctaataga agttttcaca ggaagcagca gtcaccagta gctcatctta tttttcagtt 480
 ggcaaagtgt tgtttacctt ttattggcct gcacgggtgt ctcttatcac aggatattta 540
 attagaaaac gcaagtagcc taacatagaa nagaaatggà gtggtagata atagtagata 600
 gaatggctaa atatttttat tacagtgatg taatatcact gnaattttatg gttaaaaaatt 660
 atgtaatact caaaaggaat tctcagactg gcgaaacagc tggncacag ctntcacagg 720
 gctttnanct cctnttgagc tttcccccctg ntggacttta gtcttccttt tacncccgna 780
 gtnccattn nttaccaatt gtnccgggaa ana 813

<210> 628
 <211> 646
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(646)
 <223> n = A,T,C or G

<400> 628
 tttggngngn ggtgtctcnt ttgggtggac tttttgggtc gtagggcccc aaggccgtta 60
 atcccgtaat aacggaagac gaagaagagt cagaagagtg cttctataag gatcgggacg 120
 agactacctt agaggaataa aggaaaaaag cagaggagga agagtggtag aaggagtcag 180
 aagaaaccca cactgcgttc tgaacctgga gccttatcaa aaaggtctag ataaacgata 240
 gcgatctcga tatcgagctc aagaggtagg tttagagact tctcgtcctc gagagcgaaa 300
 tggaagatct cgacgacgat aagaagttaa agtgtagagg gtgcttgagg agcgcgtgga 360
 aggattctgc ggaggggacc atcgacgtag agacttgaag gcctactaag gtccacaaga 420
 agcccggtc tttctccgaa tggtcggagc gtacagtatg cgacgtcgat cggcagacaa 480

223

gctggcggtg	gactcgaagt	gttcggggcga	atcgacttat	aatagtcgcg	cgctagtaac	540
gtaggaacac	gaagagtagt	cgaaagaaaa	cgtttagtga	gggaaaagat	tagggaaaaa	600
ggagaggctt	aataactaag	acacttgagg	cctaggccaa	cgcgaa		646

<210> 629

<211> 617

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(617)

<223> n = A,T,C or G

<400> 629

gccccnccc	ccctcctnng	gcttatnngg	acagaccac	gtagtactct	aaatcttctc	60
ctacgccgga	caacggaccc	tataccaatt	cgaatcttgg	acactccgac	cgccggattc	120
tcttcccctt	tcggcttccc	ctttctgtcg	gtacccctcc	ctagtcgtct	cctacacott	180
cgtaacgctg	atatatagtc	gccgcggact	agcctattta	ggtgtcctag	actcgttatt	240
gatccactca	ttagtctagt	actatgcgtc	acgtatctta	gttgcctaag	agggagatta	300
aatcctccac	aagttccgac	gaattcctgg	actctcgtac	tagcaaactt	tcttatgagg	360
cttcccttga	tatcttctgg	atgtttctcg	tgteccggtc	ctccgctact	actagagctc	420
cttgccctat	ctctagaagt	agaggactct	cgggttcggt	ctccaaatct	agcgctagag	480
ctatcgctac	ccgctcgatt	cccccagcgg	aatcttgaaa	cctgaggtag	tacacaaacc	540
ctcncatct	tccctcgggt	gctccttctt	ctcatccccc	cttcccgcct	tctcgggaaan	600
gaatctactt	tancttc					617

<210> 630

<211> 644

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(644)

<223> n = A,T,C or G

<400> 630

cnntcggcnt	gggttttntt	ctgagnnncc	ccccccccc	cccccccaa	cttacacca	60
ccaaacactt	tccgccccct	acctaggaga	cattagaagg	gtttaggctt	cgccgtatag	120
taaagtcctc	tacctcgga	gtagagaatt	cggtatttaa	attcagggtt	agaggctcgc	180
tcgttagatt	tatagtttag	gtttagaatc	ggaaaccttc	gatcttcctt	agaagggtaa	240
taagtgagge	cctaaatccg	tctaaccaag	gcgttaaggt	ccgtacctaa	acctagtctt	300
atcttctatc	aggegcacca	atataggtag	gttctacttt	cgtataggcc	ttaaggaata	360
gttcggtagt	tatcgaaggc	actcctctct	aggctaggct	tttctcagtc	ttagtactcc	420
gggaccgtcg	tcgcanaaat	atcgatggac	ggtaggtatc	tccgcgttac	gcgtcgggct	480
agggatatag	agcgaattat	cggcgagagg	cggtcgctan	gaatcggtat	caatatgntg	540
ttctttaccc	tacggatatc	ggcagaaaac	ataaaacctt	ctnaccangg	ataagggtatt	600
atcggacccc	taaaataaca	gtaacattta	gantactagt	accc		644

<210> 631

<211> 526

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(526)

224

<223> n = A,T,C or G

<400> 631.

ccntcgggctt	gggttttttt	ctgagccccc	ccccccccc	ccccccccc	cccccccggc	60
cccatagccc	caccggnccc	acccaaattt	taacaaaata	aatntaccta	tcgntcacct	120
atcccnegta	tcgngtaggt	cggtagccgt	accgngatc	ncnacgattn	ttcgggtcgt	180
cncctttaan	acggncccgt	agccnccgga	anaaatacta	cgagnactc	taatntagca	240
anaccgcgcg	tcnattanta	gcacccttag	tcttccaatg	ncgnggattn	ngaatacctn	300
naagttatcg	ggtagaacgg	gtcccgggtc	cccgccctct	ttncaatata	cgccgggtac	360
aaantcgggt	tctaaattcc	ncacgaattt	ngncggcaac	attcncgggn	ccttattanc	420
cntttccaac	cccgatacnc	nagctcgatc	gggctttanc	gaatccgggg	tcncccccca	480
ngantccggg	tcctttgagt	ngctctagga	cggttacgac	ggagga		526

<210> 632

<211> 647

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(647)

<223> n = A,T,C or G

<400> 632

tttggngggc	ggnggctcat	ttgggtggac	tttttgggtc	gtaggaacct	ggtaggagg	60
gtgttttgag	tttcttcttc	gtcgtctctg	ggagggttcg	tttcgattga	gattcgggtt	120
cgtctttatc	ttacgaggca	ccctgatatt	gttgcgcttt	ggtttggttg	tggagagttt	180
tgctctactc	tagcgggtca	tgcgatgat	atgtagcctg	cgtggcctga	tagtgatgtt	240
gtgagcttga	gaggggagtt	gtgggtggtg	cgggcgaggt	aggaggggtt	ggagcaccgg	300
gattgggaga	tatagaatca	taagtgttag	gtataggctc	attgagcgag	ttcgtggaat	360
tcgtgtggtc	atcataatta	gagtgaggat	gggctctata	tttcttagag	gacgcacggg	420
cgtgattcgg	ggtttgatgg	gtgttcttct	tgtgggcacg	attagcttgt	tcattgatgtt	480
aaggaccata	ctgtttcgaa	tgaggattcg	tgtcttcgga	ttgttggtga	tattgtggnc	540
tanactatatt	agtgtgaagc	ggagggtggt	tgcctgtgtg	gagtatccga	nnttcattcg	600
ganggtatgc	gtgcggagcg	gtccttgtag	acattccgga	aaaatgg		647

<210> 633

<211> 630

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(630)

<223> n = A,T,C or G

<400> 633

tccttcgggt	tgggtttttt	tctgaccccc	ccccccccc	ccccctcgga	aggcctctag	60
gtccccacc	gtctctctaa	tcctcaggaa	ccgatccacc	caaccaactt	actaatgtcc	120
tacagtaaac	accgagaat	ataaaccac	acctaggcct	ccaatcctac	caggaagca	180
agaagccgta	gtctagcgta	ttacgaaccc	gagatagaga	cggagatact	tagttttatt	240
ctctcgggaat	aggaaagacg	actggggagg	gaatataggc	tagcgcgggg	ataggggcta	300
tggcggtat	ggggcggggt	cgctctctta	ttcttctata	ccacgtcaat	aggaatgtag	360
atatacctag	atgttcccgt	agaaagagac	gttagaggtc	tccgaagcta	ttaaaggagag	420
gcgcgaagaa	acttcgtact	ctagctttat	ataggtagtc	gctctagtcc	cataagcgac	480
gagagatcta	ctagatttctg	gtatcgccgt	cgtatgtatt	cgaaatagtc	ttcttccctt	540
tttcgatctc	ctctctatac	tacatggnga	ttatagtcnt	aagatagtca	ggatattagg	600
atattagtta	tatgacgttc	gacgggacgg				630

225

<210> 634
 <211> 647
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(647)
 <223> n = A,T,C or G

<400> 634
 ccntcggctt ggggtttttt ctgaccccc ccccccccc cctccactaa ganccttaacc 60
 caaccctata gtttactcgt ataggggaat cgaggagaaa taggaacgaa gagcgggtga 120
 taaagagaaa gtactttcct ttatatgtta agagcttagc gtaatgactt tcgttatatg 180
 gctagttgat tttatccggc gttatagggc ttagttctgg ttatctcggg tctaattccc 240
 ttagtatgct cgggagttta acgaggtcac gggatagcgc gtaccctttc taaggttcct 300
 ggaaagctat tcgttattta tcgcgattct cgaggtcgaa aggatcaagg atcttccctt 360
 ttactaccct agtcgggtta gcggtcggtc aaaactagtg tagtaccttt acctcctcga 420
 aagttatagt cgaacaacag tattagtcga aattatagcg gatagatcga gacggttcct 480
 tctcgggttc tcagccggta atccctctat ttgggggtct tctccctctt cccctttgtc 540
 ttccgcctta gcttccaagg ttccctcgaa gcgaggggtt ctacttaagt cgntagcgtt 600
 ccttataaac cncctacagg cagacccctt tgtaaacggc tcggggt 647

<210> 635
 <211> 645
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(645)
 <223> n = A,T,C or G

<400> 635
 ccttcggctt ggggtttttt ctgagcccc ccccccccc cccgaaactc gccttaccct 60
 agatacccaa agaatagttc cactcaactt cgtctaagta aaactctaga acttccaaac 120
 ataaaagact tcgcgcgggt agctacacag cctacgggaa tctcacgaat cccgattcaa 180
 gtcccactct cgaccacacc ccggtatcgt cgttttcca taccaatgtc gaaaaataaa 240
 ataaaatcca gtcaagcccc acggtaagcg ggggtagggc taggcgaaga ggcaggaacc 300
 gttcgaigcc gggggctttt aaaatacaaa acaactactt aaagtttacc ctttctaag 360
 tcgggggcaa cggttaaagc acgcctctaa agtactactc gtttcgagaa ggggtagtca 420
 tctcccgcat agagactctc gcgtatatca actcgcatcg cttctagcat tccgacggtc 480
 gcccgcggtt acatatcttg cggattagct ccgagggact ataggggtta ttagtctagt 540
 aaattctctt agaggatagt cggggtcgta gttaggcagt acgaggggac atggnctgcg 600
 tcgtgctcta ccttgacagc atactcttat aaacatcttt ttcct 645

<210> 636
 <211> 643
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(643)
 <223> n = A,T,C or G

<400> 636

226

ccttcggctt	gggttttttt	ctgaccccc	cccccccc	cctagcggaa	aacaatcccc	60
accgagattt	tattaatcgt	aaaactcgcc	ttcggtagca	agtcttcctc	cttcccgtaa	120
cctggctccc	tcctagnngc	tttacgaacg	tcctctctct	tcttacggct	cggaagtggg	180
tacgggttaa	tccggaggng	gggctaacga	atccaaggct	aactcctctt	anagtttggt	240
gtccnncngt	ttagtaagga	tccgtggagg	gcgagtattt	gncccccggc	ctttattnta	300
tagttcccta	gtacgataaa	gntaccggct	atcctattac	agcggataaa	agttatttan	360
agggccgacg	tcnccgctag	acaggctaca	gctagnggag	gtaccgcctc	cgactantcc	420
gttgnntccg	acaaggngat	ttcgggttaac	tccacaaact	cctccgccga	ctctanggtg	480
gggacggcag	ttccnncgtt	tagtgtgcgt	tatagagaag	ggcatttgag	ttggacgtta	540
cnttttaaca	taggttattc	cgtttaggtt	cttgccggcc	cgtgggggta	gtncnccggc	600
gcgttnttat	cggcgatttt	ccgcagtttc	cgtttcgggn	tnt		643

<210> 637

<211> 631

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(631)

<223> n = A,T,C or G

<400> 637

gggttntctc	atttgggtgg	actttttggg	tcgtaggaac	cggtatgnag	gagtaggagt	60
cgctgggaag	actagaagtt	agctacggac	gattagtgtg	attccactct	taataacgag	120
taatcgttta	cgctgggttg	gtgtttcggg	gttttgagga	gtaagcgtag	ttgtggagtt	180
tcgcatatag	gtccccttac	ttcggcgatc	tcgtcttctg	tcggtttagt	tattattggt	240
catccttcgc	attagtagta	gggttggtcg	gataaatcga	tagctattct	ttagaattcg	300
tagtcggaga	attcgtgtac	gaagtccttt	aagttcttta	agttccgcgag	taagacgtgt	360
acggttattt	tgtcgtcgac	gtaggtgtcg	tttacgggag	tttcgtttta	ggggtttacg	420
tagaacgtta	ttaagcacgg	taatacgata	gaggattacg	cgacgtatcc	gtcttagaac	480
gtcgattttt	cgaaggcgca	tttgttatcg	aagggagtc	cttgagagaat	cgagatattc	540
caagaatatt	acggagatta	cagatcggaa	ggctcccag	atcggacgta	ttaccggtct	600
cgcccgaaac	gagtaggtat	cntccggata	a			631

<210> 638

<211> 606

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(606)

<223> n = A,T,C or G

<400> 638

cccccccc	ctcaaccatc	nattccccac	ctcaacgcga	attacggttt	cgaaagtcga	60
caataagtc	ggtcgagtag	agggaaatcag	gggctggtan	aaaggaccac	gggcggaaaa	120
taccggtctc	cttcogggga	gcgacgtcgg	ggaaaggga	gagagcggtc	tagttcgtag	180
gcaaacaggt	cagaaaagtt	aaggttaaag	gtcggagggg	agaggatagc	tagtacgctt	240
agttcggggc	tcgggcccag	ggccactttc	ctcttttcgcg	ttcctttact	ctgcttacga	300
gttcaggctc	cggagttccg	cgccggaggt	cgtcgcgacg	ctaggaatgg	ggactcgcctc	360
agtccecggt	tatccttcgg	gattctatgt	tttcgccgat	agacggagac	cgggtagtag	420
ggttcgctcg	taccgccact	cgtcgccttg	atccggccc	ctccgcttaa	gggcgatgaa	480
agattaggtg	ttagggtctc	acgggacgag	gcataggggc	ggagaagggg	ggaggggctc	540
ggggtcgaag	ggantaagaa	atcgcantcg	cgcggggctg	gtagganccg	aaatttttct	600
cnncgt						606

227

<210> 639
 <211> 592
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(592)
 <223> n = A,T,C or G

```
<400> 639
tcntcggt  tgggtttttt  tctgagcccc  ccccccccc  cccccgggaa  cgagaaaaca      60
atccccacct accgcgggga  gtgggttgna  cgcttagttc  tagaatcctc  ggaatcgtcc     120
tccggcggtg gtagttccgg  cgattccgag  tatgccgaag  tgtatcgctc  cgtctagagg     180
ttggtatctg tttatcgcg  tgacgctatt  gactcggatg  ctttcgaagt  agggggatag     240
gcgcatagat acgcctccgc  ggtgtcctct  gaagtggccg  catccgtgga  cgcagcgtag     300
acagctctgg tggacgataa  cggcttctcg  tactctact  cgggtatta  tgtagagag      360
gacttgtttc tgaacggata  taccattagc  gaagggtac  cctccgctaa  cgcaggcggt     420
tctaacagtt cttccgggcg  ctccgaattt  agattgacgc  ctccgcagca  ttgtgggata     480
ctcttcggtt agccctcttt  ataggatttc  tctccgccc  cgaaagangg  ctggtcgtcc     540
ccggcangta tgtctagctc  gaacgctttg  ttactccttt  gttttcgaaa  na              592
```

<210> 640
 <211> 637
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(637)
 <223> n = A,T,C or G

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<400> 640
ctttgtggcg gtggntgtct  catttggtg  gacttttttg  gtcgtaggct  tatccgggtn      60
gggctcccga agtagcttag  gatcgccggc  tagttccggt  cccgcccgtc  gaaagcgcg      120
ttcggcgggc ggccccgcgt  tcgttcgcgg  gctttaccct  catagagtgc  caggctctcg      180
ttcttacggg  ttcgtcgggc  atagatttta  cggcgagagg  tcggtatctt  cgccgcttta     240
cgttcggtcg gcatctacgc  ctagttcaca  ggtagtttat  gcgccggagc  gcgtgacgga     300
gaggttatac gggacgcgga  agaaccgcct  ccaaatagact  agtacaggct  cgttcgggcg      360
tagatctcct cgctcggtcg  gcggttctta  cttctagggc  cgctctacgg  tttaaggcg      420
tcgttagatc ttagaaacta  tactcaagtt  tcagtcggaa  gaaaggaagt  agagagaagg      480
gtaaacgatt acctccggtt  ctagcccttt  ttactcgcat  aacgggagaa  cggggtccgg      540
ctctcagata cgctcgcgga  gacgtcgcg  ttcaacttta  acctccgcta  ggcatccgt      600
atacggttaa cgcggtaaaa  gcgacctcgg  aaacctc
                                                637
```

<210> 641
 <211> 649
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(649)
 <223> n = A,T,C or G

```
<400> 641
ctntgtggcg gtggttgtct  cagtttggt  ggatttttgg  gtcgtaggna  acctggtatg      60
aggctagatt tcttcaacga  ttcttggtc  agttacgcga  ccctatcctt  atcttacaat     120
```

228

gtcttctaca	tcaggttcat	caattaatat	atcaattaca	cattaacgac	ggtgtgacgc	180
aatatgagaa	agtatacatt	aaggttatta	tatattattc	gcttaaaaag	gttcctgaca	240
tgggacaact	tcaccaccca	ttctagaagc	ccccctcct	gtaggacccc	ctcgagttcc	300
ccattatctt	agttcagttt	tcatttttta	accaggaggg	tatcggtttt	taataggtac	360
tattttgtca	aacttttcag	aagctttatc	ttcaaata	cttgacccat	ctgtactagg	420
agcactaact	attcgagtct	attacagctc	aacagaaaat	aattgaaatt	aaacaacctc	480
agtatcgctc	accataaccc	catcgggctc	tcaccccat	tcttcataag	ttctagagca	540
tcttgagctc	tttctatta	cccttgatgg	tactcatggt	ctaatacccc	cgcagttat	600
aggctcctat	ggatcctatg	ctaccaccgg	tctaattcct	tctatcacn		649

<210> 642

<211> 645

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(645)

<223> n = A,T,C or G

<400> 642

tccttcggct	tgggtttttt	ttcgctcgcg	gttactatta	tcgattgtta	cttgtaaagg	60
cgatactccc	accgctcacg	atattagacc	tgctcctcta	gaagcgaacg	gcgataggtc	120
tactcggccg	gcgaagacgg	cgaacgggta	ggaggagcca	tatgcaaccc	taacggagat	180
tataagtact	gggaaaaata	ctagtattaa	ggtagcgggt	taagataggt	ggagagacac	240
tattcacgag	cataagcact	tagaagggtc	tctcgaggag	aggtaggcta	cggactacgt	300
tccttcttcc	tctagcctcg	agagggagta	tagatgatcc	gcaaaagaga	atccctccta	360
tacgctggca	taactagacg	acgcgtcgtc	gggaaatctc	gccaaacctc	ttgcgacctc	420
caaaaggaag	attgtcggtt	catagaacgc	taatactccg	ggtcttcccc	aatcatagcc	480
gcataatcgg	aagaaagacg	taaaatcgcg	cgatttctaac	aagattctgt	agacttaagg	540
ctaagcacta	gaagcgatct	cgattccgga	tcttaagatc	ataactaatg	ttcgggtcaca	600
ccagacgacg	attagccact	agaagcccta	ctccgtnгаа	accgg		645

<210> 643

<211> 586

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(586)

<223> n = A,T,C or G

<400> 643

ctttgtggcg	gcggtgtctc	atttgggtgg	atttttgggt	cgtaggaacc	tggtatgcag	60
ggtccgccc	gaattaaaag	cggtatcccc	aaaacgnngn	ttcgcaagaa	gagaagaatc	120
atagcgatag	anctttcata	gtacaaaagg	aactaagagg	aaaataatgc	agattcagaa	180
ctagtgtcca	aattagaact	cgattaggcc	aaggatccga	gcctggcgct	atcacttcgg	240
gacttaagct	acggtagagc	agtcggtcct	gaagcatagc	tcccgtagga	cgtaggaaac	300
tagtccggca	cggaggacat	actctcgagt	ctcgggaacgt	ctatttagaa	tataaacgca	360
ttaacctcag	aaggcgccga	cgcggttact	ctctagggaa	ctatttcatt	cottccggag	420
ctccccatt	tttccaacac	atataccggc	aaaggaaaat	cttntgtcct	cgggtctaaag	480
agagggaaaa	aaaacgatat	ctaggttcgg	gtttatccat	ttaaaaanat	ngacgcgact	540
actccctttc	aaagggagtt	tccccctagg	nagagttcaa	cngaag		586

<210> 644

<211> 646

<212> DNA

229

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(646)

<223> n = A,T,C or G

<400> 644

ctttgtggcg	gtgggtgtct	catttgggtg	gcatttttgg	gtcgtaggaa	cctggtatng	60
agggctat	gacttgtttc	tcaaatccca	tgggtatgg	ggtggcggtg	gggggtggcg	120
tcgggttcgg	gggggtgggg	gtcgtcctcc	aaaggagttg	ctagagggct	tttagtggtt	180
ttagggcggg	aaggggttag	agcggagaga	cgtcgtcgtg	gaagcttctg	gcggagcgcg	240
agaaggtagt	tagcgccggg	tcggaagatt	ctcagaattc	gagaagaggt	agtggggcgc	300
ggagagagag	tttctaagtc	taaacgtaga	ggtcgtccta	gtcgggccc	gagtagcttt	360
taagctagag	gtcagaggtc	tcgtttaggg	tccgggctct	tcgggcagta	tcctctttct	420
cgaggaaacg	agcgaccgac	gtcgtagccg	gacccgtcta	tccgtacgtt	tagagatacg	480
ctcacctcca	cgggcgtata	tgcccgtata	cgtataaacg	cgtaatatatac	tcgcgcgtaa	540
aacacgtata	cactatatac	acgcctcgta	cggaccgtat	agcgttatatac	gcgcgcggtat	600
attaatttac	acttatatac	gcgttaacac	gatatatcac	acnccg		646

<210> 645

<211> 654

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(654)

<223> n = A,T,C or G

<400> 645

nccntcggct	tgggtttttt	tctgaccccc	cccccccccc	cccccggtcg	acaacgtgcc	60
caccgttgcc	atcccagcat	agctggttcg	ttctgtttta	ttcttagtag	tttagttcgc	120
ctatagtccc	tcgtctatcg	tctatcattt	aaggaggcgg	ggctcgctct	ttagggcggg	180
tatcttaggt	attcttcttg	tttcggctgc	cgtctcggag	tctggctcct	ttgctttcct	240
ttcttggtg	aacttcgtgt	ttgatcgcg	tgtttctttg	gggtcgctat	acctaagggc	300
cacttcgcca	acaaacaagt	ttgtgtagtc	gtttctatta	gggttcgctg	gccggcgctc	360
ttactggttg	gcgattttta	acgcgttttg	ttttaatttg	cttcctcccc	tagggctcgc	420
tcgggtcttct	ctctgttcgc	tgctctcgtc	cggccttttg	tcgggggata	gctccggcta	480
ttancgtgcc	gtgtccgtgt	ggnttttg	caatgtgaag	gcctaggggt	gcgggcttct	540
ttggccatgg	nttccccctc	tgtgancctt	aggggtaacg	antcgttaatt	naaggtcggg	600
ggttggnata	cgttntangg	gangcctgng	tccgntattc	cttgtttttg	cctn	654

<210> 646

<211> 645

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(645)

<223> n = A,T,C or G

<400> 646

tccttcggct	tgggtttttt	tctgagcccc	cccccccccc	ccccacgcc	aagtacacag	60
acccaccaaa	aacaacgtca	acacaacttc	gggtatacgg	accttaagag	agacccccta	120
gtagacccta	ccacagccat	ccaatagtca	aacaacaagg	gcgcacccaa	tccatccata	180
gagctatcaa	acaacggagg	ggaaaggaaa	gagcagggtc	aacttagcag	agatcgaagt	240

230

cggcactaat	tcctttcaag	tactcgctcg	gctttagtatt	cggggttaaag	tccgctctca	300
aagggccaac	gaggttttaa	agcgaccccc	gtatcgagtc	ttcttcgtat	tcattaaggc	360
gttaaaggta	cgagacctag	aagagagtag	aattagccca	ccaaatcgcc	taaaccggca	420
aaaacgacca	aaagtcaaag	acccttacia	atatcacctt	aaaacgcaa	ccccaaaaac	480
gcgatcagta	acgcacgtac	ctttccacg	cttttctttc	tttcaactctc	caaaacaaac	540
ccgaatattt	agcgcaaaaa	atatccgagg	gagaattaga	agctattacc	cgaaaaaaa	600
ncgganangg	antaaatngt	ggggaatana	cgtttggttt	ttctg		645

<210> 647

<211> 753

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(753)

<223> n = A,T,C or G

<400> 647

accttacctg	gtaccggggc	ccccctcgag	tttttttttt	tcacaaataca	actcagattg	60
tatacgaaaa	gctgataata	cattgacttt	tgctgtttta	atcccttgag	cctttgataa	120
tgattttttt	tgtgttaaca	attgtagtat	ataaaatcgg	attcaccatc	cttctgatgc	180
catattgatt	agtttgattt	tatggtgatg	ggatcattgt	gtgttaactg	tattaagaag	240
aaatggattt	gattgacttt	gcatccattt	ttatctgtgt	tactttcatg	ttttatttaa	300
aagcattttc	ggaccagaat	aagtttaagt	gtataatttg	ctttttacac	gtttatataa	360
ttgaagttag	caatgtggca	aaatctctaa	tggaaataaa	atgcttcaga	atgatgacat	420
aaatctgagc	tatttcttgc	ctggagaaca	agtggtattc	ataataattt	aatagcttct	480
gaggtgtttt	gttcatgtga	tgaaggctta	tccaccttgt	atcaattcat	gggctctgct	540
ttgtttaatg	tagtcagggt	gttaatacna	gacttaagag	tcactcctact	gtgataagtg	600
gtgagtgaag	attacatgtc	ttangaaaa	tatactggga	atatctctga	cattaatggg	660
tttaaatgtt	ttaaggctag	gggatgatgc	aatgganaan	atncttccaa	angtttctgg	720
ttgtttatat	ttgnggaagn	catnaagana	ccg			753

<210> 648

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 648

gatatcccgg	ggaaatgcgg	aggcctttng	gcttacgtgt	ttaccgcgta	gggcaaagcc	60
ttgncaaat	cccgccagc	ggagcggcga	gggtggggac	tcacgggaag	ttaaacagcc	120
tcgtcggcgt	cctcgaggct	ccaaaaccag	gctctaggcg	gggacgactg	cagccgttat	180
ggagggcacc	gcggctacgg	ccgcggctga	ggcctcccca	ggtggagcgg	tggcctggag	240
gggaatcttg	atcctggggc	agccacctgt	caagaggagg	cggagcgtca	tgccctctga	300
agactggatg	aatattctcc	aggagcctga	cgaaggcgaa	gaagtctttg	cagaggaaat	360
tgaatgctgt	ctgatgctac	aat				383

<210> 649

<211> 349

<212> DNA

<213> Homo sapien

<220>

231

<221> misc_feature
 <222> (1)...(349)
 <223> n = A,T,C or G

<400> 649
 cgattgtnta cnagtcttag agtaagctta agntcgn tac cgagctcgga tccactagtc 60
 cagtgtggtg ggaattccat tgtgttgggt cactagtaaa tggatttagc tagacanagg 120
 anatttacc tttccattt agcacagtga gganaggcta nacagctagg atgcaataaa 180
 aaaaatttta atgagaaatg tgtgtggttag attaatctca ttaattctcaa gttatagatt 240
 aaaaaattta agtaccncat aaatgccatt tgcctttgct aangntacat ttttatgaan 300
 aangaccntg catacnaat ganatactgg actttnggna cttgangga 349

<210> 650
 <211> 306
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(306)
 <223> n = A,T,C or G

<400> 650
 cattgtgttg ggagcctcct tccatcagct cccatgagaa attctctgtt gggtttaagc 60
 aatccccaaa tatatcatat tgacatgaat atatcatctc ctcaatgtcc agcattagca 120
 gacaagatga gtgctgaaga tgatataact cctacctctt atgtaggcta gaggtaaaagt 180
 ctggctctgc tgactgtggg gacataccga aaaggaatgt gggttaatat cagangacct 240
 ccctgcagat ccganantca gggnetggac tttctgggan aggaagcnaa aagttatntc 300
 tgaacc 306

<210> 651
 <211> 769
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(769)
 <223> n = A,T,C or G

<400> 651
 cattgtgttg ggcagggtca tttctaaggc atgggctgga agcttttatt taaaacttta 60
 catgtcttag aagcactctg gttgttgcta ggcagacaat tttacatctc ttgctatacc 120
 agttgcatga agttcatcat gcatattggc tgtggaaaac cttaacagca tcatgtcata 180
 aggtttcagt aagggtttaa tgaaatcatg tattaagcac ttagtatagt gcaccttaaa 240
 tgtagcttc aaaacaatga caacctaaact aatgttgaaa gaagcttgtg tttgtaaatt 300
 atgtcttatt gaaagatgtc atcaaactcct gttattttcta atcccttaaa gtctctcaat 360
 gtattttctt ttgccatata caatgacagg accttagttt aagccagtgg ttctctcaac 420
 ttctaatacca gagatacctg ggtgtcccca agaccttttc agagcatcct tgatgtcaaa 480
 accattttca taataatatt aaaatattat ttgctcattg tactcttatt ctctcccaaa 540
 tattcagcga gttttccaga agctatataa catgtggtaa catcttatca ctctgacgat 600
 taatagaata tngnttttg gattcttng tttaaaatt tctcactttg gggtttcta 660
 atggnnacga ttaatagata tggntccat gaccagangg ctttaaagca ntcaataatt 720
 ttttaagagac taagnactat cttttaaaga tngngaactc catcttaat 769

<210> 652
 <211> 267
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(267)

<223> n = A,T,C or G

<400> 652

nnangccctt	taaccattgn	ggcctccacg	cnntggcggc	cgctctacaa	ctagnngatc	60
cgcnaactcta	gnanaangat	tggctcttnt	gggntgggccc	ggncgggctg	gggcggttaag	120
cggggctggg	cgcgcgccgn	ggttgnacna	ggcgccgccc	cccncacacn	cccggagcac	180
cctcnttgcg	gcntntcccc	gctcaccccc	cgcgcgccgn	tccgcttttt	ccncacccan	240
agcncntttt	atctntgtct	cctccgg				267

<210> 653

<211> 501

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(501)

<223> n = A,T,C or G

<400> 653

cccnttnacc	cattgctgga	ctccaccgcg	gtggcgcccg	ctctanaact	agtgggatcc	60
ttncnatgag	atgnngcgang	gaggacnnat	ttgctatnct	ggatggggct	gantcntnta	120
gctnctctag	cancagatgg	gttatcgagg	aagatgaetc	caangggeta	nantectatg	180
cncatcctaa	aanncanctg	ctgtnttcag	agtacgcgac	acatcatcnc	tnatgcattg	240
ntgancaaga	cgggcangtg	cttatccetca	gcgangatgc	ccttaaccan	gagctcgaat	300
ggacntatca	centanaggt	acanntnccg	caccacacac	cngcttgcn	cctgacgctg	360
gactggatcn	cttaggccac	caatnccccg	tttnccacat	ncctgggacn	ctananatac	420
tcganggggg	gcccgggtanc	caattcgccc	taatactgag	ccttgntacg	nacgctnact	480
ngngtcccta	ttanaacggt	g				501

<210> 654

<211> 710

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(710)

<223> n = A,T,C or G

<400> 654

gcgnctttan	cncatgctgg	gctccacgcg	gtggcgcccg	ctctacacta	gtggatccca	60
acactgagtc	caccacagna	aaactcanca	ccaggcagac	cccacaactg	cagaatccag	120
gctgcaattc	acagactaat	cntctagacc	cacctcagta	ccagatggta	ccacacagct	180
caaggnttta	ggtttgcgtg	gtanactcaa	tctctatctt	tcaccactgc	cagcctgact	240
tcagagatcc	tgngctctgg	acagtccetca	gtggcaggca	actctcagga	gcctcaggnt	300
tttggcacat	cccagnacca	gccagctgcc	acaggccctg	acctntanc	aacactgccc	360
atgtattcca	gacttctanc	ataccacagt	gccatgctga	ttgcatctat	agangctcag	420
gtgcncctca	aanctgtgcc	tgtgcgagna	ngccccacgt	ctctggcatg	ccccaatgcc	480
atgngtggn	acanttgact	tctgggcatg	ntggaattcc	ctaccactga	ncctgaccat	540
aggnggganc	ccattttttt	cgaggggggg	gcccggcccc	caattccncc	ntatagnagag	600
ncgtanttac	gcgcnnctta	ctnggccngt	ngtttaacaa	cgtcnntgan	ctggggaaaa	660
cccctggngg	cnacccaaat	taaacngent	tgcannacat	ccccctttcg		710

233

<210> 655
 <211> 202
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(202)
 <223> n = A,T,C or G

<400> 655							
ccccttttnc	ctttcanccc	ccccggtttg	gcngccgcn	acacctactn	catccaccca		60
cantcgacca	cccagagcttt	tttccgatcc	cancatcnat	gcngattttt	tctntgcntg		120
ctgngcctgc	acctttgnta	ggtcaagcct	ggcccatctt	cgacaacttc	ctcatcacca		180
acgatgaggc	atactctgac	ga					202

<210> 656
 <211> 308
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(308)
 <223> n = A,T,C or G

<400> 656							
gctgntgaaa	gaccacaccg	aaaaactctn	ctttccgact	tccacatgat	gatcngcatg		60
tggtggtgag	agacttatca	tgacgacatc	gcttccnacc	atcgcanccn	ctgcccgaagc		120
ccattctctg	aggcctgggn	antttctgtga	ntgacntnga	cnetanacnc	tnccactgtn		180
tgctatccag	acttgnttng	aatatnttat	tggcnaaana	canttnccga	atgctgtgnt		240
tgnnccattga	angatctgat	cactatgaga	gggtgaggac	nncctgctng	ctggcantnt		300
ntaacccn							308

<210> 657
 <211> 696
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(696)
 <223> n = A,T,C or G

<400> 657							
accntttcca	caatnctgnn	ctccccgcgg	tggcgggcgc	gtcgaccagc	aacctcagct		60
gtgggtcttg	ttacagtaat	gagttactgt	aaggaaagtg	tgacatttcg	agcaatttga		120
tttgtttaaa	aactagagca	gtttcagggt	tttccttgta	aatctgtctt	atgtgtcttc		180
aatgttcttt	cttgaggagt	agagaaagga	attgttagga	atgatgcata	aaccatggct		240
tattttatct	cgtgccacc	cataatcaga	gcagattctt	gggactatga	ccctcatgga		300
gacatgacaa	ttgtgtgtgt	ggtgggtggg	agaaaagagc	tgggaatttt	tagggctctag		360
aggggtccat	caggactatt	ttatggagct	ctgctcacca	actttaagtg	agcaccaggg		420
gtgngaaagc	gaatcttggg	ntcaaaaana	caatggnaag	gggtaagttg	gtatnctgaa		480
ctggccactt	cggactctta	tttaactggg	tattctcant	taaggaggcn	nngggtgtct		540
tggcttgtna	aggaaagcct	gtgcaatgga	atgactttta	aaccccccat	taaaaaaaaa		600
angntataaa	tcttgggtct	taanaangaa	gcctgggttc	tnttanccca	ttttcccccc		660
gggaaggnaa	atnttcttag	gnaanggaag	ggaagg				696

234

<210> 658
 <211> 698
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(698)
 <223> n = A,T,C or G

<400> 658
 ctggactccc cgcggtggcg gccgctctag aactagtggg tccgtgttgg ctcaattctc 60
 aaggctgttg ctgtgcggcc tgttccccac acgtgctgct cagctcaggc aagcaccgag 120
 cttgtgttgt ttcatgctca gcgtggaggc ccctcctcca ggctgctgct ctgtggggtt 180
 cccatacact caggctccta ggaggagtcc atttagaaag ccagggtttt tctcagagtc 240
 ttagttcctt gtgctgtcat ccatttcaca cgacttgggc cctgctcggg gcaacacagc 300
 aagagaaaag acagggaaaa taagagaggg accttgcaca cacacgctct ggaccacaga 360
 gccctgtgcc cagctcctct gtcaatacag gtggaatctc gtgcaggatc gcagggggtct 420
 gtgatgccac caaagagcag gccgggacag ggtaggaga gaaaggagag ggaagtgggg 480
 gtttctccta cgcactctta tttgcagagg gaaaggcggt tttgtattgg ggttgtcggg 540
 ctttgcaccc acngcacagt tgtgagacac cccatcctn agatcaaagc cccacataca 600
 gcttggggaa aaacaaaacn aaacaaaaca aaaacagtaa acctccatgc canttgttgg 660
 gnaagttttn aatttncttc cccnaccan cttgcttc 698

<210> 659
 <211> 750
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(750)
 <223> n = A,T,C or G

<400> 659
 ncaanctggn ctccaccgcg gtggcgcccg ctctagacta gtggatcctc ctcatggggc 60
 tggatatctc tgaacatatg atgaacattg cttatgaaaa attatttgta ngaaaattgt 120
 gaggcctaag aatgntattt tcttttagtg atggtctttg tttgcttctg taaggnaactt 180
 gtgggcactc gtaagcttgg atctctttaa tctaatacca gntttgagat tttcttggcc 240
 ccatagatga attaaaactg gcgtacttct tgtttacaag anggataagt ctcctagggt 300
 aagtcttttg ggtcccaag tcaaaaagat gagggattta ccagttctct aaccttggtg 360
 gccccagact ccaaactttg ccttctagtc ccaagaggct atcaaaaagc aaaggccatc 420
 ttccaccttc ttttccanaa cagcacacat tccagacagt acttgaaagc aggaacctcc 480
 ttatccctta aaaacctctt ggaancatct tccctctctt gcttctacta tgcttggccc 540
 acctancatt cncntttttc tggaaaccgg aaaaancttn tgacttnngt tggctacatt 600
 cagcttggcc ccctacaatn tggtttccat ctgccctaan gaaattttta agggcacttt 660
 tttnttggcc cctgactttc nntttttagg gctttccccc angctttgcc cctttgttga 720
 aaggggttat tttccttccc cttttggaag 750

<210> 660
 <211> 849
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(849)

235

<223> n = A,T,C or G

<400> 660

tcggatccac	tagtccagtg	tggtggaatt	cgcggcccg	gtcgacgggc	agtagtggtg	60
tgcntntcta	aatgttataa	ttatttcaga	attactctgc	cagaaagtta	tgatcataca	120
tagaagagtt	tgtagctaac	tttgaaagta	gtggaaagtg	gttttcatgt	attgtttggg	180
ttaatttaaat	tttgattata	tttggttttt	agttcaggta	atTTTTttgt	tgaaaacttc	240
aaatgacaat	ttcttcatgg	ttactaaaga	tcactcatgt	ggagtagttt	cagatttttt	300
tctgaataca	tgtattactt	ttagagatgt	aaagatgtga	aattactaag	agagaaaccc	360
atgtgatttg	tttagtggtg	caaaagtcgg	tagctccttt	gattcctaag	gccactgata	420
gttaaataga	tactgaagct	atgggcaggc	tggttgata	agaaaaaagg	agacagagaa	480
atgggaaatt	gggaaagaac	tgtgcaata	ggaaaaggag	agagcaacag	aacagaatta	540
gtaccacagt	gccgaagtgc	cacctcaggt	acttccatct	cccatctcct	gaagaattca	600
gtaacagttt	gcaaatggtc	aacacaatca	tttagtgatc	ctggttgata	ttttcaatac	660
tttctgggga	tttcttggtc	ggnttcaaaa	gatgatgctg	atagttttat	tgccctgaa	720
ggtattctga	agnttancat	aatttattgg	tcagtaaaat	atttgaataa	aagngganga	780
aggaaaatct	ggcntcttat	tttgggatnt	cngcnggggg	aangaggata	taattnacc	840
cggccttgg						849

<210> 661

<211> 653

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(653)

<223> n = A,T,C or G

<400> 661

aacttaagct	tggtaccgag	ctcgatccc	tagtccagtg	tggtggaatt	cgcggcccg	60
tcgacctcca	ttcgtttctt	gtcctttttt	ttcatttttt	ctcatgttct	attcacttta	120
ggttttctaag	ataaatatta	taaaataatt	tttacttata	aattattcac	tgataccctg	180
tctttaacat	gtgaaatgaa	ttcaaaaagga	atcttaatga	gaaataatat	actcatgatg	240
tttaatatagat	ttgatttcga	aataataagc	cctctgaagt	cctaagttaa	aaataaagca	300
acttgtttga	taatttttca	tcaagaatgt	atctgagtct	ctgagtaatt	attagtagga	360
atattccatt	atcacaaatta	cacagtataa	gctatttagt	ctaactttac	caaaaaagg	420
agctacttca	acactgtgtg	agacttttaa	tggttttgca	ttgggtatgc	actattagca	480
agataaccta	ttttacagca	gtgtttntta	acctttccca	tttatttgaa	aggcagctaa	540
gatatagtag	ttaatntaan	gggctgatgc	atztatatta	catgtagana	atgggagata	600
cnaaagggag	nggggggana	tnttttgnat	tcnnaagctt	cnttgncaat	taa	653

<210> 662

<211> 646

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(646)

<223> n = A,T,C or G

<400> 662

aaacttaagc	ttggtaccgc	agctcggatc	cctagtccag	tgtggtggaa	ttcgcggccg	60
cgtcgaccga	gggacaggca	gccagngctg	gggtcaccag	gggtccctct	tgggccctcc	120
aanagcaaca	gtactggcaa	cagctgggat	ttgctgagca	cagactctgc	agcaggctcg	180
gttgagctct	ctgtgcctgt	tccttcatac	catcctcacg	cccatccatg	agatgggtcc	240
agctgttttc	agatgagaaa	atggcacagg	aagctggtaa	gtgacagtca	gaaatgaatg	300

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ctggcagctt	antccttga	cccaccgcag	tgcaggacct	tgctcaacag	ggatcacccct	360
tgctccgccac	ctgttcatga	ggccacccag	ggtttgtgtg	gtcatttgtc	tcctttcatc	420
tgcttgccctt	caaccagctg	ggtcattagg	gctggggaac	ccagacccca	cacagtcctt	480
ctcccagang	ccagacacan	nctncgccac	agnaaggact	tcagtccccg	aancaaagt	540
ncctgggcgt	anaaactgna	gggncccca	tccttgggtg	ggtactgctt	tgcaactggng	600
gaattcaccc	ctcattgnna	acctttccct	nttnncccc	ctaaac		646

<210> 663

<211> 650

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(650)

<223> n = A,T,C or G

<400> 663

aacttaagct	tggtaccoga	gctcggatcc	ctagtcagct	gtggtggaat	tcgcgccgc	60
gtcgacgtcg	acgcggcgng	ccgtttcgac	gcagttgata	catattatta	tatactacat	120
nggttttcta	gaattaaaaa	attaatgtgt	agtgccagcc	ctagatgtaa	gttacatata	180
tcaactctat	ccaattttgt	cagccataaa	acttaccttt	ttcacatact	tctaactcta	240
acaatgtgag	aaatgtagat	cattgcaatt	ataccacaaa	ggcagatggc	tacatgcaga	300
atggatagca	gaatctagct	acttacgcta	gccacatggt	agacgttttt	tcctttgttt	360
ttgcaaaatt	gcaatataag	ttgcataatc	ttagagtga	aagatgtaa	gaaccatag	420
aagccagtga	tgaaggacat	ttatatattc	acctttacaa	angaccttaa	aattgcctat	480
gtggagcaga	aactggagga	gggcnaancc	atcngtaaaa	aaaattttgn	tncattttgg	540
atgtgggcac	cattattacc	tcccaggtt	cctttttgnt	ttaacctttc	ttttaaaaaa	600
aataattcnt	aatttttggg	caaaaaaaaa	caagggtttt	attfaaattt		650

<210> 664

<211> 678

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(678)

<223> n = A,T,C or G

<400> 664

taaaaaatcta	gactacacta	ggaaattatt	ttantatcag	aagaatatca	ggggtgtagt	60
actcatcana	gctaaatgag	agcgctttaa	aaatgttagt	ttgtcttccg	ccatttctac	120
agaaagctgc	aatttcaggt	tttcaacctt	ataggtgata	tttaagaaaa	aaaaaaagca	180
atcgcaaata	gccccactgc	ttttacaaat	cattttttct	cttctaggta	tagcctgtca	240
ggtggccata	tgtaattttt	gacatctcta	ggaattttta	tagaaccaga	aatgggtgcc	300
agagatatgc	ctgcactaat	cttaagtggg	gatttatgta	tttctcaagc	aagtgattaa	360
agcaaaacta	ggcacgattg	aaatcaanat	cttttaggca	agaaagtcac	gatgagtttt	420
anaattattt	taggactctg	tggctttctc	ttcatagaaa	tagaaaaaaa	aaattgtata	480
aaaaccacaa	aaggctctga	atagcccaaa	gcaacactga	acaaaangaa	caaagcagga	540
agcaacacac	taccggaatt	caattatact	accaaggtgt	antaacccaa	acagcattct	600
attgggcata	aaatagacca	aagaccagtg	ggaaacagaa	taaagaancc	caaaataaat	660
cctatatatta	cngcccn					678

<210> 665

<211> 694

<212> DNA

<213> Homo sapien

237

<220>
 <221> misc_feature
 <222> (1)...(694)
 <223> n = A,T,C or G

<400> 665
 ctttttcaaat cattttttnct cttctaggta tancctgtca ggtggcctaa tgtaattttt 60
 gacatctcta ngaatttttaa tagaaccaga aatgggtgcc agagatatgc ctgcactaat 120
 ctttaagtggg gattttatgta tttctcaagc aagtgattaa agcaaaaacta ggcacgattg 180
 aaatcaagat ctttttaggca anaaagtcac gatgagtttt agaattattt taggactctg 240
 tggctttctc ttcatagaaa tagaaaaaaa aattgtataa aaccacaaaa ggtcctgaat 300
 agccaaagca acactganca aaaagaacan agcaggggaag caacacacta ccngaattca 360
 aattatacta ccagggtgta gtaacacaaa cagcattcta ttggcataaa atagacacca 420
 agaccaatgg ancagaataa agaaccacac aaataaatcc atatatntac cgccanctga 480
 ttatcaataa cnaacaccaa gaacatatnt taagggacnt nctattcaat aantagtgtc 540
 ggnaaaaact gggaaatcca tatgcagaaa naatgaaact agacccttat ccctcaccat 600
 acgcaaannt caacttcgga atgggattac aaaacttaag acattccaac ccaagaaact 660
 atnaaancta ctattaagaa aacagatcnc nccc 694

<210> 666
 <211> 705
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(705)
 <223> n = A,T,C or G

<400> 666
 tttaaaaatt tagatacact angaaaatta ttttagtata agaagaatat caggggggtgt 60
 agtactcatc agagctaaat gagagcgctt taaaaatggt agtttgtctt ccgccatttc 120
 tacagaaagc tgcaatttca ggttttcaac ctaatagggtg atattttaaga aaaaaaaaaa 180
 gcaatcgcaa atagcccccac tgcttttaca aatcattttt tctcttctag gtatagcctg 240
 tcaggtggcc taatgtaatt tttgacatct ctaggaattt taatagaacc agaaatgggt 300
 gccagagata tgcctgcact aatcttaagt ggggatttat gtatttctca agcaagtgat 360
 taaagcaaaa ctaggcacga ttgaaatcaa gatcttttag gcaagaaagt catgatgagt 420
 tttanaatta ttttaggact ctgtggcttt ctcttcatag aaatagaaaa aaaaattgta 480
 taaaaccaca aaaggtcctg aatagcccaa gcaacactga acaaaaagaa caaagcagga 540
 agcaacacac taccagaatt caaattatac taccaagggtg tagtaaccaa aacagcattc 600
 tattgggcnt aaaatagacc naagaccaat ggaacagaat aaagaaccca aaataaatcc 660
 atatttttac agccagctna ttatcaataa aacnccaag aacnt 705

<210> 667
 <211> 817
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(817)
 <223> n = A,T,C or G

<400> 667
 nnangacttt tgtggtntta tacaattntt ttttctatct ctatgaagag aaagccacag 60
 agtcctaaaa taattctaaa actcatcatg actttcttgc ctaaaagatc ttgatttcaa 120
 tcgtgcctag ttttgcttta atcacttgct tgagaaatac ataaatcccc acttaagatt 180

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agtgcaggca	tatctctggc	acccatttct	ggttctatta	aaattcctag	agatgtcaaa	240
aattacatta	ggccacctga	caggctatac	ctagaagaga	aaaaatgatt	tgtaaaagca	300
gtggggctat	ttgcgattgc	tttttttttt	tcttaaatat	cacctattag	gttgaaaacc	360
tgaaattgca	gctttctgta	gaaatggcgg	aagacaaact	aacattttta	aagcgctctc	420
athtagctct	gatgagtact	acaccctga	tattcttctg	atactaaaat	aattttccta	480
gtgtagtcta	aactttttta	aaaagacatg	taatccgctg	agtttgtaac	tcaaaacgag	540
tgcatctagg	aggtatcgca	agccgtttct	ggattaaatt	cccagctagc	ttgcttgctt	600
agcaggggcg	ggnaaanaag	acatctgcag	cctagggaag	aaaacctttc	gcattgttct	660
tacgtgttta	cgttatttta	tttctanaaa	caaggcngaa	ttgggactcg	aatgggtcag	720
ttgggggtggg	ggatcccctg	gtncataaaa	ngtcanaaag	anggtacagg	cggaacncca	780
agggtcgctcc	tgcatttana	ctcggaattt	tggtgcc			817

<210> 668

<211> 826

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(826)

<223> n = A,T,C or G

<400> 668

cggggggnnt	tacgtctctc	tggacgcttt	tattgtacca	gggcgatccc	agcccaactg	60
taccattcga	gtccctactc	ctgccttgct	ctagggaat	aaaataacgt	aaacacgtaa	120
gaacaatgcy	aaagcgtttt	cttccctagg	ctgcagattg	tcttcttcac	cgcccctgct	180
tagctagcta	gctagctggg	aatttaatcc	agaaacggct	tgcgatacct	cctagatgca	240
ctcgttttga	gttaciaaact	cgcgagatta	catgtctttt	taaaaaagtt	tagactacac	300
tagggaaaat	tatttttagta	tcagaagaat	atcagggggg	gtagtactca	tcagagctna	360
atgagagcgc	tttaaaaaatg	ttagtttgtc	ttccgccatt	tctacagaaa	gctgcaattt	420
caggttttca	ncctaatagg	tgatatntaa	gaaaaaaaaa	acaatcgcan	atagcccact	480
gctttttacaa	atcattttttc	tcttctagg	atagcctgtc	aggtggccta	atgtattttt	540
gacatctcta	ggaatttttaa	tagaccagaa	atgggtgcc	gagatatgcc	tgcaactaatc	600
ttaagtgggg	atttatgtat	ttctcaanca	agtgattaaa	gcaaaaactag	gcacgaatga	660
aatcaagatc	tttaggccag	aaatcatgaa	nanttttana	attattttan	gaatctgtgg	720
cttctcttct	taaaatngaa	aaaaaaattg	tttaaaccca	naaggtctga	ataccaagc	780
ncctggaacn	anagaacaan	gccggagcac	cccctcccaa	atcccc		826

<210> 669

<211> 547

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(547)

<223> n = A,T,C or G

<400> 669

cattgtgttg	gggaaaaaat	gatttgtata	agcagtgggg	ctatttgoga	ttgctttttt	60
tttttcttaa	atatcaccta	ttaggttgaa	aacctgaaat	tgacgctttc	tgtagaaatg	120
gcggaagaca	aactaacatt	tttaaagcgc	tctcatttag	ctctgatgag	tactacaccc	180
ctnatattct	tctgatacta	aaataatttt	cctagtgtag	tctaaacttt	tttaaaaaga	240
catgtaatcc	gcggagttag	taactcaaaa	cgagtgcac	tnggaagtat	cgcagccgtt	300
nctggatnaa	attcccagct	tgctngcttg	ctnagccggg	gggcggtnaa	aaaaacatct	360
gcagcccnng	ggnaaaaacc	ttcgcatgtg	tcttacgtgt	ttacgttatt	ttatttccct	420
nnagcaaggc	nggganttgg	ggactcgaaa	tggtacagtt	gggctgggga	tcgcccttgt	480
tacataaaaag	ncgtccagaa	gagggacggt	tacaggcnng	ganctccaaa	ggtcagttccc	540

239

tgccatt

547

<210> 670
 <211> 232
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(232)
 <223> n = A,T,C or G

<400> 670
 cgaactatatt agactaccta ggaaaattat tttagtatca gaagaatata aggggtgtag 60
 tactcatcag agctaaatga gagcgcttta aaaatgttag tttgtcttcc gccatttcta 120
 cagaaagctg caatttcagg ttttcaacct aataggtgat atttaanaaa aaaaaaagc 180
 aatcgcaaat agccccactg cttttacaaa tcattttttc cccaacacaa tg 232

<210> 671
 <211> 214
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(214)
 <223> n = A,T,C or G

<400> 671
 ctccccttcc ntccctcgct actnncatt ttcnnaaatt tntttcgcnt atgnggaaaa 60
 acaccacat tnttcanctc gcacagaaca ngngggggtg tgtaaaatga agggcttccn 120
 cnctttctct tattnaanaa cactnaaana gggangggct aaaaccgcg ngatntctac 180
 nctatcgcg ggcgttttgg ngttggctag aaga 214

<210> 672
 <211> 328
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(328)
 <223> n = A,T,C or G

<400> 672
 ngancagcgg ngttttaaag ggcctctaga ctcgaggaga cncctgttgg atggtggatc 60
 acanntcgnt actactatac aggacagagt atcggganct cttgngtgtt ggngcctgcc 120
 aaccactgct nctgttaact gcgtatctga agggactcgg actggcttca gaagaactac 180
 cggctogaat gnaccatgga tgattcncnc tagttgaaaa aaaactcagg cacatgtatt 240
 gccactgatg actagcgcca gactnctctc ggctctntaa cgagcccaca tgncngtgtg 300
 ncncccgtgc tgnctccaga agaggttc 328

<210> 673
 <211> 223
 <212> DNA
 <213> Homo sapien

<220>

240

<221> misc_feature
 <222> (1)...(223)
 <223> n = A,T,C or G

<400> 673
 gggggcaaag ctggctagcg tttaaactta agcttggtac cgagctcgga tcccnagac 60
 attgtgcatg aaaatgcaa ttgagtgtgg tctatantgc catentcacc tncctgncngc 120
 tcaaaacaac ngctttctgc tgcaatgggt agggctcctn acncacggtc gcnnacggag 180
 gccncttat cctctcgggt nnggatccct ngaagcatnt tct 223

<210> 674
 <211> 256
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(256)
 <223> n = A,T,C or G

<400> 674
 gnggggtcnt ngatgagcgc gcgtaatacn atcactntcn ggcgngntgg gtaccggggcc 60
 cccctcnaa gcggccgccc ttttttntt ttttttcatt acatgataa ntctttnttc 120
 taaacagacc acaccactan agttcctttt ctttngtacg gaattgagtt aaagtagagn 180
 atacaatgca gggcttcnnc tctatttcac attccaggnt ggttcngnat ggatcggccc 240
 tgcctctccg atgggt 256

<210> 675
 <211> 439
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(439)
 <223> n = A,T,C or G

<400> 675
 nnactagtcc agtgtggtgg aattccattg tgttgggctt gtatggggtt ttttgtctag 60
 ttntttggga aatgttngtg ttactatntt ttggatatna tatatgatat gtatggccct 120
 tctatgggct cctcanacng aactcaacca ttttccacaa aaccnattcc tcctttccct 180
 tcatgactga gtggtgttgg tactatccng gaaactggga cattgtcctt cacatctntc 240
 ccttanctgc ctngtccnat tgatgtcttt gagctntgan atgtctttgt taactntctc 300
 ctncntctgt actgccggca naattaagca ccatntgtca caaaaagtat tgcgttacct 360
 tcacgnatct gttngttnc atncttgctg cttctccngn ggaaaatagg ctnttctggc 420
 aaccgaacng aanaaatac 439

<210> 676
 <211> 587
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(587)
 <223> n = A,T,C or G

<400> 676

241

nggnggcctn	attaagcgcg	cgtaatacna	ctcactntgg	ggcgaattgg	gtaccgggnc	60
cccctcaagt	tnatntgcn	aacctctctt	ttggaataac	aaaagggtta	acacatatgt	120
cctcataggg	acgcgctttc	acacnttcc	gacngcttca	tanacntcat	tnctatttct	180
cctcagnaca	agttnaggcn	gaaggtgagg	canacnttat	aatttccatt	tcacaaatnc	240
ggaaagttag	gctcaaagg	nttaaaaaat	aacctgatac	aantcataga	gccggtnct	300
ggaanaagca	ggagcaaagt	ccaggcatcc	tgatccaagc	tnggtccact	gccttccact	360
ctggagaggc	ttcatctccg	acaaaggaag	ggacntgagt	ggctgganaa	tctcatggga	420
taaagacctc	agnatttcat	gctcctggaa	atcccatggg	ttgaacaaca	ggtntttggc	480
ccgtggttct	ntccctttgn	ccatctttta	accttggggg	aaatgatggc	ntctntnagc	540
nttttttttn	aaagagatng	aaattgaatg	attatnngct	cattggg		587

<210> 677

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(444)

<223> n = A,T,C or G

<400> 677

gtggggcatn	attaagcgcg	cgtaatacga	ctcactatag	gggcgaantg	ggtaccgggc	60
ccccctcgaa	gcgccgcgcc	tttttttttt	tttttactgt	ccaaactntc	tatngatnta	120
gttgaaactgt	ncaacgattt	catgaaattc	tatacacana	gccttcaggt	ccagagagta	180
aaacaaattt	aaatttnttc	accanattgn	agcagncana	agcatccnat	nataccgac	240
tacaatgaat	natatgctna	nggtanctna	tttaccact	ntgggggtctt	tanggtctgt	300
cacaaactat	tttcgtaaac	atcnntttta	anttnggtga	atggacctaa	tnccagataa	360
ntctatttna	tntacccatg	catncctgtg	gctnactttt	cgggctgtgt	tggentactt	420
ttaggagaaa	attggtataa	atnn				444

<210> 678

<211> 670

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(670)

<223> n = A,T,C or G

<400> 678

actagtccag	tgtggtggaa	ttccattgtg	ttgggagcag	tttaaaaaaa	aaaaagacna	60
aataatacnac	tcttgatnaa	acataaagg	acagtgggtct	atgaggaana	gaaaaggtag	120
ctnaggatgc	aaaantacct	accacatggg	aaccgttngt	ccacactcat	tccnnaaaaa	180
accgagtcct	ctcanttnca	cacgtgtacg	tttcagttgg	gaagtgtctg	ccattactcc	240
naagcctaga	accttcacgt	cctgaagggt	ctggaagggt	tttcagattg	cttaaganac	300
gngcccttc	catattcntc	tccactaccc	nggggaacgg	aacaaatgga	gctgcgacng	360
ggaagcgccc	cttcccntcc	gaacgcttcc	tttcaaacct	gcctgccttc	cnggcgaatg	420
gaccggaagg	tttncntngt	tcctttcanc	ccnaattact	tcctgngttg	aaaattggcc	480
tgttgggttg	caaagtgcng	aatttggtta	ctttcntcat	gtcctgtgtt	gmncaaccg	540
gctcncttgt	tgcctccctt	tngaaagggt	ttcatcaggc	cccgcccttt	ctcttntaan	600
ngtcctaate	cggncnggac	cactcgggga	aaattttttc	ttttcgaaaa	gccgccccnt	660
ccgtccggct						670

<210> 679

<211> 449

<212> DNA

242

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(449)

<223> n = A,T,C or G

<400> 679

actagtccag	tgtggtggaa	ttccattgtg	ttgggagtag	gtctactaca	ncctacttcc	60
cctatcatan	aaganccttan	caacnttcat	gatccccccc	tontanncct	tttcctcanc	120
tgcntcctag	tcctgtttgt	cctnttccta	acantcntaa	ganagatnac	taatnctact	180
atctctnacc	tccggaanct	acaanacgtc	tggaactatt	cngaccccat	gcancncat	240
ntcccatcgt	cctcccagcc	cctncccttc	ctttacntta	ctnaacgaag	gtcgcagatc	300
cctcccntac	ctcccnnc	attgggnccc	aanggnactg	gacctcacga	ntacaccnac	360
tacggggnga	ctaagnctgn	aactccttac	atatntcccc	gttacccecn	gaacncagcg	420
aacngcnaca	ccttggaent	caagaanta				449

<210> 680

<211> 670

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(670)

<223> n = A,T,C or G

<400> 680

tttcngtgtg	gtggaattcg	cggccgcgtc	gacgagaaga	nggaggagga	naaggagaag	60
gagaagaagg	agaanaagga	ggagaaggag	aagaaggaga	agaaatcatc	atcatcatca	120
tcactgtct	ngcaactatt	taagtttgc	antcccttga	aaacagggtac	ttttgtttca	180
atgtttggga	ccactnctga	cnatgannag	aanaccaata	aatgcttgat	naatgaaaaa	240
nccacttttt	acctgttaga	accctgaggc	taagagaant	gatgtgactc	gacttagtta	300
ccacaaacta	tgatcctagc	atnaattggg	gcactctcaac	acctcaactc	cctgtgcaag	360
aacagatttt	caatgtctac	tgatgatttt	aaatggatta	nttcctctct	ttacttctta	420
agggcatgaa	gntttatgaa	acaaaactat	ncagttccag	acgtttaacc	cacatagtgt	480
taatagtccac	cttcaacaca	cnactaaacc	cccaaaaaan	gntttttacg	gngtttcgac	540
agttttcttt	tccttttgac	ttgnttaaca	cccnnagaca	ctttgtntcn	tttccttgaa	600
tcacancttt	cnaanancca	atggtncggg	tttttctent	tcngggccct	tccttnttn	660
aaaaccan						670

<210> 681

<211> 494

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(494)

<223> n = A,T,C or G

<400> 681

tcattgtgtc	cacagtctga	tgtgagcgca	ttaaatttaa	ggatctccgc	ccttctcctt	60
aaaactcagg	acttggaat	gancctagga	agcgccctc	ccctcccan	ccanaccaa	120
gccccggacc	gctgcgnctc	cagctgcgcc	tagtgaaacc	gccgaattcg	aattcacact	180
cggngggccg	gcgaagggtg	gcgcgccgc	gggagcgccg	gggcnagccc	gagggactgc	240
aagccaanaa	nggaggcatg	ggtagggggg	ggcgccgtct	gatccaggaa	ggagcgagg	300
cgccgatcac	acactcttna	gacgcctgc	ccgcgcctgg	ccagcgcgca	gnctgcagg	360

243

```

cgcgcgaggc aggaactcgc tggagtttgc caagccccc gncctctggaa agtntgtagc      420
tccctttcgg ancgncctct ctggcccttt gggacgggtg tgtcattggg cgggggtctg      480
tataaggggg ggac                                     494

```

<210> 682

<211> 263

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(263)

<223> n = A,T,C or G

<400> 682

```

tgatcattca agcgnatgnc gnataacgat tgctnagccc aacctttcat agggtcgttc      60
ctttgggaat nggatgtcta ttgaatggca gggatagggg cactcggcat tcgcctctgg      120
tacagttttg catatatatc ctcatcgcca gcgagcgtag gggancgtta agtttgggga      180
aatgccnccg catgncctn ccggagctta aacccccaac aatnccatt ttnaaaaaag      240
ntttnttant taaaaaaaaa aac                                     263

```

<210> 683

<211> 255

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(255)

<223> n = A,T,C or G

<400> 683

```

cttgcccggc atgcacagac ntntttacgg acacnctact ccaagngagc ctgnanctgt      60
ctacgggtcaa nctctaagg tngncantgc cacanatggc atagtccga gggcggtan      120
totggantgc tctctgcact tgaacntaaa gcgcntttca aganaggnc atngcctgc      180
ctcttgacaa cnaacaancc cacaccnacc tangaccctn tangcaagga ctggattctg      240
naaatgcaat acaca                                     255

```

<210> 684

<211> 922

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(922)

<223> n = A,T,C or G

<400> 684

```

acccttcatt tcattgtgct ctattttcct acatctttta catgactaag ggattaatga      60
aatcacctct tcataatcat gaccataatt tcatccaaca agtactcaag tttggtgta      120
gcactttatt aatgcttacg aattctctct ctctccctct ttctcttttc cttagtcctt      180
gcacaataag gatttttgaa tgtataatat catcttaggt aagctttcat atggttttgg      240
catatgaagc ttatgactgt cataagccat accaagcctg tggagtatgg catgattttc      300
attacataat ccaatgaaaa tagacttatt ttaaattccct aactttgtag ttttaatttg      360
tatttcacta tcttgaaatt aacagctagt acttatccat cacagcagtc tcctactgac      420
atgaagcaag ttgttgaaat cagtaganca tgaatgaaag catttaatgt tanacaaaaa      480
tgggtgatac ccaagcattc tgaattattt gcataagga atgggacatg tacattagt      540

```

244

```

gcatcatttc taccaatatg tgacttgaat tgttttttta aaaaaaggan aatgantttc 600
tcaatttgct ttaaaaaatt ttnaaaaagt tcaatggcat gctgctttgt ctggacttaa 660
tttattaaca attnttaanc cttccttaag gacanaattt tgggtgttcag gatcncctcg 720
aagggtctta tttttntan nattccaaac ccaaaagggtg gtttaaaatg gnggggttcc 780
ccccncaaaa atttgaccg gcttttttat atttaaaaaa nttncnttt gngtttgaaa 840
nctnaatacc aattaagggg gaattttacc tnccagtggg aaaaaaaaac nctngccntt 900
naaaaaattc ccnggagnca at 922

```

<210> 685

<211> 531

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(531)

<223> n = A,T,C or G

<400> 685

```

tgaggctctg taaaactggt cctctgctag gcatacttca tattctctat attaaactca 60
tctttaattg gcatggaaga ttcatgttgc caaatctcag atgaagatcc tatattggat 120
gcaattaagc ctggcagcgc cctcaaaaga cagtcttgtc actgctagcc acagccagga 180
cacagtaaca gttccttcta gtgaccnag accataanaa atananatct aaagaattct 240
gactccaaag gcattagccc attcctggta ttgccaatta tgatagaaaa aattgccaag 300
ctcctgggac atggaaatac actcagtaca ttgagaact ggagaactan tttccaaaat 360
agtatgaaga catganggtg attgtagata tntgagtttg gagaanttga gggaaatcng 420
attacacatg tttactacaa gagatgttna taagtaaaga aggcctgata tacaatctaa 480
cagaenatg agataaatct taantcacia ctgaentccc ttttggggcg g 531

```

<210> 686

<211> 336

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(336)

<223> n = A,T,C or G

<400> 686

```

gngnccfna tgagcgcgcg taatacgatc atatagggcg aattgggtac cgggcccccc 60
tcaagaacac tacaagctat gtcctcttct canagagccc tgaantttta acatattgaa 120
agctctnatc ttgccaaana actccactta acttcaaaac acaccctcca cacacatcat 180
gatcaactna gatcttactg aaccagaatc ctnaatggca tacttcagga acaggggtcc 240
anagaagcag ttctcaaant gcagctnaaa aagaaactga aaaccaatt catgcaanac 300
ctagggctta tttgagagca ttttccagtg cagatt 336

```

<210> 687

<211> 271

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(271)

<223> n = A,T,C or G

<400> 687

245

aatctgcact	ggaaaatgct	ctaaaataag	ccctaggtct	tgcatagaatt	gggttttcag	60
tttcttttta	agctgcactt	tgagaactgc	ttctctggac	ccctgttcct	gaagtatgcc	120
atttaggatt	ctgggttcagt	aagatctcag	ttaatcatga	tgtgtgtgga	gggtgtgttt	180
tgaagttnag	tggagttctt	tggcaagatc	agagctttca	atatgttnaa	acttcagggc	240
tctctgagaa	gaggacatag	cttgtagtgt	t			271

<210> 688
 <211> 740
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(740)
 <223> n = A,T,C or G

<400> 688						
tgatgaagcg	cgcgtnttac	nactcactat	nggggccaan	tatgggtacc	gggnccccct	60
cgaagcggcc	gccctttttt	tnnttttttg	tgagagttta	aataaaatat	ttgagtttta	120
tttaaagtgt	gagtttaatt	aaaatatatg	gcatatccca	agttgggctt	tgcanaaaaga	180
acacttctca	ggaactgtta	gttgggtgtac	caggaactca	gaagggtcct	gttattaaat	240
atatttgga	aatgcatgga	ttctctgaan	atcncctctg	atgtgagcaa	cacttacatc	300
ncaaaccaaa	attggcattg	catacatnaa	ccaatatttc	ccaaacattt	ctgggttatgg	360
cccacccctt	ttgtgtanta	cttattgctg	ttttttggaa	ccctggggaa	attacttaaa	420
atattcagct	ggaaattaca	ggcgttactt	ttaaggganc	aagaattaca	gtgactccca	480
aaattgcaag	tggttgattac	tatttaagaa	cccaagaatt	tgaaagaaat	tttgaaaagt	540
gaaaacngga	aatnttaaat	gacttctcaa	atittgaaaa	ctcnggnaaa	catctccact	600
ttggtnccct	tccttttaaaa	attggctaaa	aattntttnt	tatnccacc	ccattggaan	660
tncccccccc	ctggaacaat	tggattcccc	tatttcttaa	aaaacggccn	cccccccccg	720
gngaacncc	nacnttttgn					740

<210> 689
 <211> 635
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(635)
 <223> n = A,T,C or G

<400> 689						
actagtccag	tgtgggtgga	ttccattgtg	ttgggattac	atatactttt	agcaattttt	60
aaagaagtgt	acaaagttag	gatgtttcct	gagctctcat	atatctgana	atgtcatttt	120
acatctccgt	cttcacctct	caaaacttct	ttcaattctt	tggtctttaa	tagtaatcaa	180
cacttgcact	ctggagtcac	tgtaattctt	gtccttttac	agctacncct	gttattttcca	240
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<210> 690
 <211> 3923
 <212> DNA
 <213> Homo sapien

<400> 690

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247

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tacctaagtc	atgtgggact	taaaacctag	atgatgggtt	gatagggtgca	gcaaaccact	3840
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<210> 691

<211> 882

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(882)

<223> n = A,T,C or G

<400> 691

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aaaataaaaac	tagtataagg	atagaagccc	agggttgatt	taagtctgcg	gaaatcataa	180
accataggtc	agacttctca	ttgatgaggt	acttggtggg	tagaatacaa	ttaggtatat	240
ttggtctaga	aaccaggatg	gaattagaga	ataaaagact	gagcaatagc	atgttatagt	300
attagaaata	ctatagaaat	aggaaaagcc	ctgattatga	ctttggagtt	ctgatccaac	360
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gtcaattcca	gttctaaaat	tccatcactg	ngcactaagg	caaattgaat	tgaataaagt	540
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gacgcantca	tccagncatc	tccatccctg	ncccatgncn	tatgtagana	tgtanctcta	660
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tggtctactt	tnaagactca	tcttcaacta	ctgggcacca	aatncctacc	attgcatcaa	780
actgggggtc	ccatncaagg	caaaccctgn	gaaatcttta	atcccgaaat	tggcgcccaa	840
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<210> 692

<211> 235

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(235)

<223> n = A,T,C or G

<400> 692

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cttctcanag	cacttaatat	gttaatatata	aactncngna	aaaaagatnt	tcnatgaanc	180
nttctcttta	ggaggtcagg	ngagaatagt	gttaatgnca	ttaagganag	aacga	235

<210> 693

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 693

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taatgcaccg	catctacatt	cccatgctct	ctttacttct	tcagcattgc	ctaaaggcat	180
aatacacctt	taattaatta	attcagcctc	ctaatagcaca	ttaacaaagc	ccctgctaga	240
ctctgtccat	aatggnaaac	ctgnatgatc	cttgatatta	acantttaag	gaatgctcat	300
ggattggttn	cagacttaaa	aaattgaggg	ggctgaanaa	aatctaangg	anaaatcatg	360
gaagcatttg	cacatattac	ata				383

<210> 694

<211> 204

<212> DNA

<213> Homo sapien

<400> 694

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aagaaccctg	tctgatgaag	catcatttca	gaattttaag	tcaacttaca	aatgtggtat	180
tattcacatc	tgagtacaaa	tta				204

<210> 695

<211> 670

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(670)

<223> n = A,T,C or G

<400> 695

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gaacggtgac	ctccaaaaga	tatgtccacc	tggaacctca	gaataagatc	ttatttgga	120
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ccagaggagg	agacggaggc	agagacaggg	ccaccagag	gaggagacgg	aggcagagac	300
agggccaccc	agaggaggag	acggaggcag	agacaggggc	caccanagg	aggagacgga	360
ggcagagaca	gggcccacca	gaggaggaga	cggaggcaga	gacagggcca	cccaaaggag	420
gagacggagg	cagaanacag	gcccccccaa	agaaganacc	ggaggcanaa	aacagggcca	480
cccanaggag	gagacggagg	canaaacagg	gcccacccaa	aggaggagac	ggaggcaaaa	540
cagggccacc	caaaaggagg	aagccggaag	gaaaaaacag	ggccccccca	aaggaggaag	600
ncggagggn	aaaaanaggg	cccccccaaa	agngagaaaa	ccnggnaggc	nanaaaaccn	660
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<210> 696

<211> 317

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(317)

249

<223> n = A,T,C or G

<400> 696

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gccactgtc	atcgtggata	catttcactt	ttttcacatg	actaaggagc	tctccggagt	180
gaagagttag	taaatatggt	tattacgcat	tcatttgcta	agaatcatca	agaacccaaa	240
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ctggatctgc	tggtgcc					317

<210> 697

<211> 246

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(246)

<223> n = A,T,C or G

<400> 697

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ggatcctcnn	anagcggacg	cctactacta	ctaaattcgc	ggncgcggtg	actttttttg	120
tttttttctt	tnacagagnt	ntttttgtgc	ccttggttct	tatgctcana	ctcngcaaaa	180
aanatcaaaa	gntacnnatg	aaaaacntat	nccatctnca	naaaggaggt	gnagntatta	240
ctttct						246

<210> 698

<211> 3674

<212> DNA

<213> Homo sapien

<400> 698

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agccagtga	acatattcct	tcttctctcc	atcaggccaa	atcacgggtg	tgaccttggc	180
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250

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<210> 699

<211> 2051

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (2051)

<223> n = A, T, C or G

<400> 699

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tgatcccaa	gactcagcat	ccaaggctcc	ctccaggaat	cctggcagct	cagcatactt	180
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<211> 2841

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(2841)

<223> n = A,T,C or G

<400> 700

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<210> 701

<211> 3228

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(3228)

<223> n = A,T,C or G

<400> 701

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<210> 702

<211> 4894

<212> DNA

<213> Homo sapiens

<400> 702

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259

```

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```

<210> 706

<211> 123

<212> PRT

<213> Homo sapiens

<400> 706

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Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe
                    5              10              15
Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val
                20              25              30
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
                35              40              45
Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly
                50              55              60
Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu
                65              70              75              80
Tyr His Arg Glu Lys Gln Val Leu Ile Gly Gln Trp Val Glu Ser Gly
                85              90              95
Trp Glu Gly Trp Ser Gly Phe Leu Gly Gly Gln Leu Ala Gln Asn Leu
                100              105              110

```

260

Val Ser Gly Lys Gln Leu Trp Arg Met Leu Leu
 115 120

<210> 707

<211> 150

<212> PRT

<213> Homo sapiens

<400> 707

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 5 10 15
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30
 Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
 35 40 45
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Glu Ser Leu His Pro Pro
 50 55 60
 Ser Phe Leu Phe Gln Ile His Ala Thr Trp His Val Gly Gln Glu Tyr
 65 70 75 80
 Leu Cys Pro Gly Ser Cys Leu Glu Gly Glu Val Val Cys Trp Glu Gly
 85 90 95
 Ile Ala Gly Gln Glu Gly Asp Pro Gly Leu Arg Gly His Thr Lys Arg
 100 105 110
 Lys Lys Arg Ile Pro Arg Thr Tyr Pro Ser His Leu Trp Ile Pro Gly
 115 120 125
 Pro Ala Gln Ser Leu Ala His Arg Arg His Trp Arg Asn Ala Pro Asn
 130 135 140
 Leu Trp Leu Ala Leu Leu
 145 150

<210> 708

<211> 371

<212> PRT

<213> Homo sapiens

<400> 708

Met Leu Phe Pro Ser Phe Ser Arg Ser Leu Val Pro Leu Pro Leu Ala
 5 10 15
 Leu Tyr Leu Ser Gln Pro Leu Thr His Thr Thr Ser Leu Leu Ala Gly
 20 25 30
 Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala
 35 40 45
 Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp
 50 55 60
 Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala
 65 70 75 80
 Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
 85 90 95
 Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val
 100 105 110
 Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro
 115 120 125
 Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu
 130 135 140
 Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser
 145 150 155 160
 Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Cys Leu Phe Gly Leu
 165 170 175

261

```

Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala
      180                      185                      190
Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala
      195                      200                      205
Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe
      210                      215                      220
Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg
      225                      230                      235                      240
Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp
      245                      250                      255
Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu
      260                      265                      270
Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg
      275                      280                      285
Arg His Tyr Asp Glu Gly Lys Ala Leu Ala Ala Ser Arg Gly Trp Cys
      290                      295                      300
Gly Ser Arg Pro Pro Glu Thr Thr Leu Gly Ala Val Ser Gly Leu Val
      305                      310                      315                      320
Pro Leu His Pro Gly Pro Asp Phe Ser Val Arg Lys Val Gly Met Asp
      325                      330                      335
Pro Ile Cys Ile His Gly Phe Ser Trp Val Trp Asn Ile Ser Ala Cys
      340                      345                      350
Gly Phe Arg Lys Ala Ser Gly Cys Ser Arg Ser Leu Ile Arg Val Val
      355                      360                      365
Ala Pro Val
      370

```

<210> 709

<211> 141

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(141)

<223> n=A,T,C or G

<400> 709

```

tacggcgtgg tgcggagggc ggtacccac aaataacacn nacaccccat cctatctgtg 60
tccacanata aantgactca ttcctctcct cgcatanccc actntcccct ngcgataccg 120
taacnaance cttccccctt t
                                     141

```

<210> 710

<211> 196

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(196)

<223> n=A,T,C or G

<400> 710

```

cnatccttcn cntacaccca tgangtccat gtgcacgctc cacctcccct caaaacttgg 60
gtccncatcc acccgctact ctcccntaa ncnataaccc cttttngcga atagacccca 120
ccttancaat nggttttctn tttttgtcc ctnggnccgn gcgattcaan aaattgaagg 180
cccanaaaaa cccctt
                                     196

```

262

<210> 711
 <211> 177
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(177)
 <223> n=A,T,C or G

<400> 711
 ntacntcnc tccnaatgaaa ttcgaanctc gggtaccg gggnaattccg attaggngcg 60
 tantctcgga tgtgcagtca caagtctttt gctaattctt ataattntcn ctaccctttc 120
 ttcnacaata ctgctatcct anttnttctn tcnctctctt cccannttac taaccac 177

<210> 712
 <211> 185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(185)
 <223> n=A,T,C or G

<400> 712
 aaacgnacca nngccaacga tangtggttg nggttggtgc ggttggttctt cttatntgca 60
 ctggttggtc gtgtcgacac ganggccacg tccctctgnc ntgagtanca catagcatcc 120
 acgttttagtc gactntnccg ggcggccgct ctaccctntt atngattctt attaaaantc 180
 ggatc 185

<210> 713
 <211> 172
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(172)
 <223> n=A,T,C or G

<400> 713
 nntggctgcc tgnccgtnta ctctaaagga tntactatnc atatggantc naanacgact 60
 cactacacgg cncctctnccg agccnnggtc agtgccctnct nggagacctt ctctggggca 120
 ggangagcac tnggtatggt cacgtatcnc ttcntaaana tacnncctc cg 172

<210> 714
 <211> 112
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(714)
 <223> n=A,T,C or G

<400> 714
 nttgcgtgcc tggacgtnta ctctgcanga tctactactc atgngaattc taantacgga 60

263

ctcactatncc ggcanccgag gcgcagcagg gaanggggtca cctcccagtc tc 112

<210> 715

<211> 326

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(326)

<223> n=A,T,C or G

<400> 715

tactctanag gatctnccng tcatntggat tctatntcga ctcactctag ggctcnagcn 60
gtcngccggg caagttattc ggatcgctcg gntccgagct tcgcaattaa ntgtgccatc 120
gttctncaac gttcctgact nggaancccc ngcngttcng atccnccngt acctagctcc 180
anntcccccg tntccttctt ggngtntcat naangaggac cncctctgat cnccttctc 240
taatctgcnc acnctgaacg nccaatggac atngtgcggt taatntanna ggcccgnntc 300
gngtgccctt ccogtnannt cagctc 326

<210> 716

<211> 122

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(122)

<223> n=A,T,C or G

<400> 716

nntgcgtcgc ctgngcgtnt actctagatg atctgantag tcatatggat tctaatacga 60
ctcannatag ggctctagcg nggatncnga ttogtontcc ngattcantg acnccgggtan 120
ca 122

<210> 717

<211> 203

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(203)

<223> n=A,T,C or G

<400> 717

cntgcatgcc tgcagggtcga ctctagagga totactagtc atatggatcg agcggccgcc 60
cgggcagggtg tnaatgataa anatgcatca tactanccta cagaanggag agataatgtt 120
ngntggacca ngttggtttt cttgcgtgtg tgtggcagta gtaagttatt agtttttana 180
atcantaccg ccctccgcac cac 203

<210> 718

<211> 168

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

264

<222> (1)...(168)

<223> n=A,T,C or G

<400> 718

```

ggcagganga tcncttgagc ccngagggtc gaggtacag tgagccanga gtgcactact 60
gtnnccgcct ccgcatncac gngtggtccg atccccgggt accganctng anttcactgg 120
antttttttt aancgtnttg antggtacna ccctcgantc cctggctg 168

```

<210> 719

<211> 210

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(210)

<223> n=A,T,C or G

<400> 719

```

cancgtcgnc ataacacgta tttntgatn aagattctna ctgacccatn aantctacnt 60
ctcaagctct tncanngtcc agtnaangga atgtgtatnn gtnggggatnc cacanaaaaa 120
aganatntcg gncgcttcat tantcatcct tcttaccan ntctctngat nencagtntg 180
ancntgaacg cacactacng gatntctcca 210

```

<210> 720

<211> 131

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(131)

<223> n=A,T,C or G

<400> 720

```

tccatcctaa tacgactcac tatagggctg ccaacctgcc atccactact gaggaagacc 60
cgnanactta ggggctcact gcgagccacc ggccacaggt cgtatagggc aaagcacgng 120
gaagcaccct t 131

```

<210> 721

<211> 121

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(121)

<223> n=A,T,C or G

<400> 721

```

tccatcctaa tacgactcac tatagggccg ntgantnctg gcgaaaggct tacaattaag 60
naggaaaaan ganccaacaa ctaaaaaaaa nncggncgtg ncagcttnga tgactngtcc 120
a 121

```

<210> 722

<211> 246

<212> DNA

<213> Homo sapiens

265

<220>

<221> misc_feature

<222> (1)...(246)

<223> n=A,T,C or G

<400> 722

```

anctggagtc gcgcgctgca gtcacattgt ggatccanaa aatcggcaca agctctcntg 60
gnttcntcga tatgaanaac actaatccca tgtngtntgn gtctccgtga ttcacccctc 120
gcacnggtcc ccntccnaac cnttgcatag gtgttatgtt gtantctccc cagtgcacaa 180
agattnacac tctctcantg tctganatat gcacgagttc attgtcctgt cnccgtnaac 240
atcaag                                     246

```

<210> 723

<211> 160

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(160)

<223> n=A,T,C or G

<400> 723

```

cctccggaat atccaantag agtaantncn ctctaattccg gggnaattgg nggggttnnat 60
acgtcctcct cccccagnt aggattnana aaaggntcc cagancaaaa nctccaaagt 120
gnatcnanta gccgtncctg ananccaacg cccctacgtc 160

```

<210> 724

<211> 156

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(156)

<223> n=A,T,C or G

<400> 724

```

tnanccnata tacaccaaata tctgattcta aantcccacc caagggaaaa aagttgagaa 60
gagcctttcc actttttctac taataaaaaa atgcaccagc ccctaccann agtgnggaaa 120
acctccttag gcccttgnnt ggaacaancg aaaatc 156

```

<210> 725

<211> 347

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(347)

<223> n=A,T,C or G

<400> 725

```

aganggttnt atncatgctg tactcgcgcg cctgcagtcg acactagtgg atccaaagaa 60
ttcggcacga gagacggtgc gcgatggacc gagggcccca gccgngagg cgccgcccgc 120
gagcccgagg ncagacgccc catcagtagc gtccgcaccg ggnagccgcg gntctcgccc 180
gagccgtggg gcgcgccgag gggcggggtc gcctcccgcc gtccctcgca gctctgccgg 240

```

266

gcccagagccc ggcgcgtcgc cgcgcgcgnc ttgcgcgtcg gncgcgcggg nccggnaaac 300
gcggtcgagg tctggatgng gcanngcccg cncctntcgc tgagcct 347

<210> 726
<211> 162
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(162)
<223> n=A,T,C or G

<400> 726
ttgggtgggt tgggtggggg naaatttncc catttggtg gggttggggg ggnaaataact 60
tccgccttt tnggtnccca aaganacnaa gggggagtcc cttnatagag gnagngcgat 120
nntcncaac nactngact ttgnccatgg ggagnaaggt gg 162

<210> 727
<211> 120
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(120)
<223> n=A,T,C or G

<400> 727
gtgtgggtgg ggaattccat tgtggttggg ggnaaatctc cgcttgtcca aagnacaggg 60
ggggtcnctt anagnnagg gggttcctcc ccaccacttg ncttgnccat tngagnaag 120

<210> 728
<211> 130
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(130)
<223> n=A,T,C or G

<400> 728
gaccactgc agcgttnaac ttagcttggg ccgagctcgg atccctagtc cgtgtgggtg 60
aattccatgt gtcgagagag gggcaaatac nctccaanac ancncctca tgctcnacac 120
atattcgcat 130

<210> 729
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(182)
<223> n=A,T,C or G

<400> 729

267

```

cngactgctn gcgtttaaac ttaagcnagg taccgaacgg ggatnnacga ctantgatcg 60
gctggctgct tccagtcgat tanatttgtg aaaaagctga accncngccn gttaaggggg 120
annatgcaaa anatncatcc nnctgccccn taaactgntc tntccnaggg aaaaaangga 180
ag                                                    182

```

<210> 730

<211> 678

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(678)

<223> n=A,T,C or G

<400> 730

```

cactcncact ccggacctag gcncttcacc actgctctct tectctctct cctcctctct 60
ctcggggctg ggggaccttc ccagtgacc atctcacttt ggctgaancc cactcggggc 120
agcctgagtt tggggctctt ggccttctca cctctctcgg cccctcctt ggcccgacc 180
aggccaaacc ggggcagccg taccttgagc ttgtgtccgg cctctccctc cccctctgcc 240
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gcagaaagta cgctcggccc ctgggggctg ctctcagca ccctcgcccc ccaccctagc 360
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cgctgtgccc tctcggctta gccccacgtc caactcaagc tggggcactg tcacggtggg 480
catcttaaag acaccctcac ccaccagcag ctcaccacct gcaacctggg ctccaggcaa 540
aaaaagggtc acctggggca nctgaaccct gtacctgtg tgccctctgc tgaanggaat 600
gttatctgaa cctgctgccc tgggggtact gccttcccaa aaccgggtca antccacctg 660
ttggaaggna aatncccc                                                    678

```

<210> 731

<211> 135

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(135)

<223> n=A,T,C or G

<400> 731

```

gagatccgac gtcacccccct tccggcggcc caagacgctg caactcccga ggcngcccaa 60
atatcttttg aagagcgctc ccagcccaac acaatggaat tccaccacac tgggnntagtg 120
gatccgagct aagcc                                                    135

```

<210> 732

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(660)

<223> n=A,T,C or G

<400> 732

```

gcttggtacc gagctnggat ccctagtaac ggccgcccagt gtgctggaat tcggctttct 60
tcaatcagnt nacgagctgc atggtctgct aacattgtca taattgctgg catagattac 120
tgaaaataaa gaaaaaaaat tgaagctgcc tatcaagttt tggattattc aaaaacttcc 180

```

268

```

tacaagttat tttacttcaa ccatgttatt acaaataatt taatgaatac tttagagact 240
ttaattacaa aaaactgaga tagtaaaagc aagtaataaa agctgaaatt acttagctat 300
ttgataatta cataaattat tatgggccat tcaacttttc tagtgtttag tttatacacc 360
aggaagactt tcctattcta ctaacattta taaagtatgc taacctatta tttaaacgca 420
tccactatta ggattttatg gcctaaaacg tgatacagtt cagtatcttg atgtcaaaac 480
ttttaagca agtagggatt aagttcaagt gaatgtgatt ttctttcttc ccagtagggg 540
cttctgaata actcagnaaa gctcacttcc attatcttac tttataaaaa aatgctataa 600
gacagaatgg gccgacgtgg nggctccacc tgtatccacc tttggaggcg agnggcgaat 660

```

```

<210> 733
<211> 836
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)... (836)
<223> n=A,T,C or G

```

```

<400> 733
aattaatgac tttttttccg ccctgccaa ctagtttgtc taaatataat gtaaagaaat 60
tagctactca ttttctgggc cacgaagggt cctaaaatgg gaagaagtgg agatctgacc 120
ttgttagttc taaatacact aaactgggag tgccatggat ggctttcagg atgtcctgaa 180
tcctctataa ttgtatacaa aatcgtgagt ttttaaaaaac tgggttagag ctattgggtc 240
ctcagagtct caggcatctt agaccccaa aaaggttaag gactactgac ttaaccaatt 300
aggtttgagt ggcattgggt ttgaagaaaa gcagaggaaa gatataattt ataattctgg 360
gcaacaaaaa agtggatgtg tgccagcatc tttagtaga atcctcttaa aaggatagca 420
ctgcatatga actagtaggt ttaaccagt gcatatttag gcgaagtagc tcatttttct 480
gttagaattc ttttttattt gggaatgggc aagcttttac agcttttacc ttgccaatga 540
atacctggaa tttaaaaaat cttgttaggc atattgcca taaagttttt tttcctagat 600
cataattcca gtaaataatg ttgtagcttt atttcaatcc cccaattcat tgaggggtga 660
aacaatttga atggtttgag tgtagaagct aagttatttc tgtagaggct aagggcattt 720
ataccaanat atgttagact tgnngntcct gttaaccatg ctgtanacaa taggaattac 780
tgtatatcca cattttaatt ttaacatctt ctgctttgnt gntggtttga gangga 836

```

```

<210> 734
<211> 694
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)... (694)
<223> n=A,T,C or G

```

```

<400> 734
nagtnctatt tncactaaac tngnagtgcc ttggatggct ttcaggatgt cctgaatcct 60
ctataattgt atacaaaatc gtgagttttt aaaaactggg ttagagctat tgggttcctca 120
gagtcctcagg catcttagac ccccaaaaag gttaaggact actgacttaa ccaattagggt 180
ttgagtggca ttggctttga agaaaagcag aggaaagata tattttataa ttctgggcaa 240
caaaaaagtg gatgtgtgcc agcatcttag agtagaatcc tcttaaaagg atagcactgc 300
atatgaacta gtaggtttta accagtgcac atttaggcga agtagctcat tttctgttta 360
gaattctttt ttatttgagg atgggcaagc ttttacagct tttaccttgc caatgaatac 420
ctggaattta aaaaatcttg ttaggcatat tgcccataaa gtttttttct ctagatcata 480
tattcagtaa atatgtttgt agcttttatt caatcccca attcattgag ggttgaaaca 540
atttgaatgg ttttagtgta gaagctaagt tatttctgta gaggctaagg gcatttatac 600
caagatatgt tagacttgtg gttcctgtta accattgctg tagacaatag gaattactgt 660
atatccacat tttatttttt aacatcattc tgtc 694

```

269

<210> 735
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(126)
<223> n=A,T,C or G

<400> 735
ncnttgaaac nggttgacca gacttcaggc ctgtgcgctc aatcgtggag aatctcgtgc 60
cgaattcggc acgagtctct ctctctctct ctctctctct ctctctctct ntctctctct 120
ctctct 126

<210> 736
<211> 165
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(165)
<223> n=A,T,C or G

<400> 736
cagaagcctt taaaccggtt ngaccagact tcaggcctgt gcgctcaate gtggagaate 60
tcgtgccgaa ttgggcacga gtctctctct ctctctctct ctctctctct ctctctctct 120
ctctctctct ctctctctct ctctctctct ctctctctct ctctc 165

<210> 737
<211> 125
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(125)
<223> n=A,T,C or G

<400> 737
ggnagcccct ttaaccgttt gtccagactt caggcctgtg cgctcaatcg tggagaatct 60
cgtgccgaat tcggcacgag tctctctctc tctctctctc tctctctctc tctctntctc 120
tctct 125

<210> 738
<211> 137
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(137)
<223> n=A,T,C or G

<400> 738

270

```

ggagnncctt gancaggatg accgacttca ggcctgtgcg ctcaatcgtg gagaatctcg 60
tgccgaattc ggcacgagtc tctctctctc tctctctctc tctctctctc tctctctctc 120
tctctctctc tctctctc

```

137

<210> 739

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(970)

<223> n=A,T,C or G

<400> 739

```

aggcctattt aggtgacact atagaacaag tttgtacaaa aaagcaggct ggtaccggtc 60
cggaattcgc ggcgcgctcg acggcccttn gtgccactag ntctttcatt cttccccccc 120
atcaatcagt gaacttttta gcctactcaa agctttgctc caatgcatag gatttatgat 180
tgtggggatt tccagataat ataaatattc aacatgaata ttttaaatga aggcattgaga 240
catttttctt aactgagcat agccatgaac ctctcacgtc tgttcctctg tgtcagtttg 300
tancactgaa tacagcagcc ctctctctctc tccaggcagt gcacaggctc tgacatgatg 360
aagtgcgctg ttgctatggt gattttgcag ctggccaaat agtcactggg tgattttacc 420
cagcaggaga tttttgcaaa aatttcctgg gtgagagtga aatcaaactc ctattttgnt 480
tctcctctgc aagctgnagt taagatggat taatgagtac ttttagatta attaactctg 540
aagagaaaat gggagaaaag tgaggaaggt tggttggcaga agtcattgct ggaatccttc 600
tgaagggagt actgacttca cttgcaaaga cnagagacta naagacaatg aagttaaact 660
tggcctgtct ctcatatgat agatgctgag agtcaggntc agggaaattt aattctgtca 720
tacgcataatn ggattatgtg gtcattggatt tggttggcact aaccngcctn taatcagnat 780
aagaaaagtg ttttggtaga naaagaaaat tatggcccag aaaaacctgg aanacttggg 840
aaaaatgntn gggggccttg ggtgggtggc tnaaaanacc ccctggggat ntttaaacca 900
aaantgaaga agggaaaaat ntttcccnt nttttntttt tttgccccct tgggattggg 960
ttttntttcc

```

970

<210> 740

<211> 739

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(739)

<223> n=A,T,C or G

<400> 740

```

gntgtcnaaa aagcaggctg gtaccggctc ggaattcgcg gccgogtcga cggcccttgg 60
tgccactagt tctttcattc tccccncca tcaatcagtg aacttttttag cctactcaaa 120
gctttgctcc aatgcatagg atttatgatt gtggggattt ccagataata taaatattca 180
acatgaatat tttaaattaa ggcattgagac atttttctta actgagcata gccatgaacc 240
tctcacgtct gttcctctgt gncagtttgt agcactgaat acagcagccc tcctaaaagt 300
ccaggcagtg cacaggctct gacatgatga agtgacgtgt tgctatgggtg attttgcagc 360
tggccaaata gtcactgggt gattttaccc agcaggagat ttttgcaaaa atttcctggg 420
tgagagtga atcaaactcc tattttgttt ctctctctgca agctgnagtt aanatggatt 480
aatgagtact tttagattaa ttaactctga agagaaaatg ggagaaaagn gaggaagggt 540
gttggcagaa gtcattgctg gaatccttct gaagggagta ctgacttcac ttgcaaagac 600
aagagactan aagacaatga agttaaactt ggcctgtctn tcatatgata gatgcttgag 660
agtacaggnt cagggaaatt ttaattctgn catacgcata ttggattatg tgggtcatgg 720
ctttgtttgg cncctaacc

```

739

271

<210> 741
<211> 1171
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(1171)
<223> n=A,T,C or G

<400> 741
gccttgnggt gacactatag aacatgtttg tacaaaaaag caggctggta ccggtccgga 60
attcgcgccc gcgtcgacgg cccttnntgc cactagtctt ttcattcttc ccccccacatca 120
atcagtgaac ttttttagcct actcaaagct ttgctccaat gcataggatt tatgattgtg 180
gggattttcca gataatataa atattcaaca tgaatatttt aaattaaggc atgagacatt 240
tttcttaact gagcatagcc atgaacctct cacgtctgtt cctctgtgtc agttttgtagc 300
actgaatata gcagccctcc taaaagtcca ggcagtgcac aggtccttgac atgatgaagt 360
gacgtgtttgc tatgttgatt ttgcagctgg ccaaatagtc actggttgat tttaccacgc 420
aggagatttt tgcaaaaaatt tcctgggtga gagtgaaatc aaactcctat tttgtttctc 480
ctctgcaagc tgtagttaag aagggattaa tggagtactt tttagaatt aaattaacct 540
cttgaaagaa gaaaaaatgg gggaagaaaa aaagtggag ggaaaagggn ttggttttgg 600
gccnaaaaaa aagttccaan tttnggcntt ggggaaaaat tccccntttt ccttggnaaa 660
aggggggnaa ggttaancct tgggaacctt tttccnncct tttnggccca aaaggggaac 720
ccanggggaa agaaccctta ggnaaaggaa acccatttgg gaangggttt naaaacnntt 780
ngggcccccg ggccctcttc caanaaggga aaaaaaaagg cctggaaaaan gtaccagggt 840
ttcangggna aaanttaaaa ttcttgccca atanncctat aattgggaat tatggggggg 900
ccatgggctt ttggtttggg cnccttaaccc cgcnttttaa attcaaanna aaaaaaagng 960
gtttggaaaa nnaaañaaaa aaaattnaan ggncccnaaa aaaaaccctg gaaaaccttt 1020
ggaaaaaaat tngnnggggg gccnttttgt tggggggggt tnaaaaaacc ccctnngggg 1080
ttttttaagc ccaaaagggg gggaggggna aaanggtnc cttntttttt ttttnngccc 1140
cccttgggga atggnnttant tcanggggcc c 1171

<210> 742
<211> 739
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(739)
<223> n=A,T,C or G

<400> 742
gntgtcnaaa aagcaggctg gtaccggtcc ggaattcgcg gccgcgtcga cggcccttgg 60
tgccactagt tctttcattc ttcccncca tcaatcagtg aacttttttag cctactcaaa 120
gctttgctcc aatgcatagg atttatgatt gtggggattt ccagataata taaatattca 180
acatgaatat tttaaattaa ggcatagagc atttttccta actgagcata gccatgaacc 240
tctcacgtct gttcctctgt gncagtttgt agcactgaat acagcagccc tcctaaaaagt 300
ccaggcagtg gacaggtctt gacatgatga agtgacgtgt tgctatgggt attttgcagc 360
tgGCCaaata gtcactgggtt gattttaccc agcaggagat ttttgcaaaa atttctggg 420
tgagagtga atcaaaactc tattttggtt ctctctgca agctgnagtt aanatggatt 480
aatgagtact ttttagattaa ttaactctga agagaaaatg ggagaaaagn gaggaagggt 540
gttggcagaa gtcattgctg gaatccttct gaagggagta ctgacttcac ttgcaaagac 600
aagagactan aagacaatga agttaaactt ggcctgtctn tcatatgata gatgcttgag 660
agtacaggnt cagggaattt ttaattctgn catacgcata ttggattatg tgggtcatgg 720
ctttgttttg cncctaacc 739

272

<210> 743
 <211> 610
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(610)
 <223> n=A,T,C or G

<400> 743
 ctgtccttat ttcttttagca aaaatttccc aagagaagaa ttgctgggat aatgcacatt 60
 taaatttttg atagacattc ccaaataatta tacctgtttt tgagacctt aattcctgtt 120
 gtcaaattgc cctatatatg gagtaataaa cacgatttaa agaaatgagg actaaaaaaaa 180
 gattatatat aacccaacat aaaggcaacc tcttaggcgt tgacagaaac tgacaacttt 240
 ttatctgtgg gtgcgatcca ttataagtaa cctgagcacc ttattttttc tttttaaaact 300
 ctaggttagga tacccgaggt ccacaaattt ttcataagaa atattttttc tctgccctat 360
 gagatttttaa aaaatattat actgcttcaa ttgcatcaaa agaaatggac cctaatatct 420
 atgatgaagg atttgaggtt agaagacctg agtttcaatt ttggcatggc tgtttgtcta 480
 gctctngat cttggacagg tcaattgact tggcttaatc ttctcatcca tttagnngag 540
 acagcaccac tattcacagg actattgncn gaattaccag acaatagcat agngaaaaat 600
 ataangcctt 610

<210> 744
 <211> 127
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(127)
 <223> n=A,T,C or G

<400> 744
 ttnacctccc tggaccgggc ccccttccc cgggcggntc ccccgggctg caggaattct 60
 gcacgagga gagagagttt gagagagaga gagagagaga gagagagaga gagananaga 120
 gagagag 127

<210> 745
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(458)
 <223> n=A,T,C or G

<400> 745
 gatatcccgg gattcgcggc cgcgtcgacg tggcctctag tttgtcctgg tccaaagcag 60
 ggaagctggg ctacgtcctg cccaggtcag ccttaggtta agggctgcct gggggagga 120
 acttctctgg ccttcgggtc tctgtgcact ggggtggctc ctgtggccca gaatgccctg 180
 gagaagggtc ctactggaag cgaaggtgca gggcagcagg gcctgaggcg caggagctgg 240
 tggaggctcc cagcacaggc cgccgcccca gtcacatcac tgctgatggt ggggggactt 300
 ggggagtttc ccccgagaat gggaggtctc acagtccccg tgctgcaatg ctgtcgggtc 360
 actgngncng caatgtgctc atggncaactt gctttttctc tgtggccccg gccgatttat 420
 ccagcanngc acccctcttc tncctccgg anaaagcc 458

273

<210> 746
 <211> 893
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(893)
 <223> n=A,T,C or G

<400> 746
 aagcaggctg gtaccgggtcc ggaattcgcg gccgcgtcga cgtggggagt tagctctctg 60
 gaccccgctca tagagtaagt catcgataga gcatttgctt gatggggact tccagaaggc 120
 canngaaagt cctgccgact tcctggggaa gcccatccgc acgtgggggtg aggggtcccca 180
 natggaagca gctgtgtatg caggggagggg gcagaggctg ctgccaatgg gcatgtccct 240
 tacctgaaag ggccacctct ccaggtgaca tgtcctgggg gagccggggc cgtctgtctcc 300
 ggccagaggc gctcagctca ggccacacca ggcagggcac ctcccaacct ggacagggtg 360
 ggaccaaggt ggccttggaac aaaactctct gtgtttgcc aagcaccat cggacacaga 420
 gagtcaacca caccacagtc acatggtgtc cacacngcag ggtcaagga ggcccgccc 480
 ctccccctca gacgtccctg ggctctctgg agtcagcaag gacgaggacg gcattgccct 540
 tcgagacagg aaggggagtga cctcctcccg gcggcatcca ggctcngctt ctccggagag 600
 gagagggggc tacttgctgg ataaancggc cggggccaca gagaaaaagc aagggtgacca 660
 tgagcacctt gcaaacacag tgcacccacc agcatttnag caccngggac tgtgaagacc 720
 tcccatttct tcggggggaa acncgcccac ngttcccccc accntcacta gtgnattgtg 780
 acctgggggn cgggccgacc cctgtngctt gggnnagccc tcncccagg tttctnnggc 840
 ngcccnttaa nggncctng nttggccctt tggcncctt tncgcttttc cca 893

<210> 747
 <211> 738
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(738)
 <223> n=A,T,C or G

<400> 747
 gatatcccg ggaattcgcg ccgcgtcnac gaagcacaga cctgngccct gctctcatgg 60
 ggcagactgc catttgtcat tnattactga aggaaagga tcctcagttt gcttgtggac 120
 atttcaaatt tgagggtgaga gttggataag taagaataaa gctgctcttc aaagagatga 180
 atatagaaaa agaaacaaga tacagncttg gcagtaaggc tgggaggaag gggaaaaggt 240
 aataaagaat gaaagagtga gaaatgtgag caggagctga acacagaaaa gttcagngac 300
 agaagcanaa ggagggaaga agggaggagg gtccctttca cagaggctca cgaggatgct 360
 ttatgngtgc catgcagtcc atgttcagga tgtctgcttc ttanctctct acttttctaa 420
 tanaaatttg gatacttact gatcctacat atgtaacagg gagagaaggt gaatttcaa 480
 gcantaaatt gaaaaattgt tcacaatttc attttttaaa aaaaggagc taacagaaga 540
 agagggttaat gtggttaatta taggatgnct cttgcgcacac atgaatgnat ctggtatcat 600
 ctgagtggga ggggagctgt cttcctgacc caaaaggatc ctttcgttan ccngnactta 660
 ngtcccaaaa cctcaccacc ttggagaaat natttccttt tgggggtntc attaaancct 720
 tttggncccc gcaaaagc 738

<210> 748
 <211> 647
 <212> DNA
 <213> Homo sapiens

<220>

274

<221> misc_feature

<222> (1)...(647)

<223> n=A,T,C or G

<400> 748

```

ctntgtggcg gtggctgtct catttgggtg gacttttttg gtcgtaggaa cctggtatng 60
aggtcgagag taagacgggc tattagtagt cgcacgagag ttatttgtga aaacctggtt 120
agggcctctg tctccgctgc gctcgctaa attggtatgg ctcgacttgg aaacacggtt 180
ctaacacgcg ttgttagcgc ccttgctagc atgtgaagga cactggccct accaagaaag 240
attcgagtcg ctccctccgg tatcggtcac ggaggcgata ttactcttct ttactacggt 300
tacttcgaga ttgtctgtga agtttaagac tactaaaaag agtattaagc ctatcgggaa 360
ttagctagat cgacacgcta aaaccaaggg caatcggcgg aaatatagag gcaccaataa 420
tagggcctac agaaggcccg agggtagac tcacgtttaa taccggccac gggagaaata 480
aaaagataaa gtatacatcg tttagcggtc ctcggaagcc ttcggcttta atgccaagga 540
gtcggaagca tcgtcggcga gtaataaact ccatcgcgcc gagactatct acgacgccct 600
ccttaanatc cgtaaattac tcccggaaag agtatttagg cggctct 647

```

<210> 749

<211> 642

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(642)

<223> n=A,T,C or G

<400> 749

```

ctntgtggcg gtggntgtct catttgggtg gacttttttg gtcgtaggaa cctggtatgc 60
aggtccgcgg agcgtgggct ctcgctgtgg atgttggggg ttggtgtggt gccggttgtt 120
tttggttctg ttgagcgtag tgtgtttgaa ggtagcggtt cgtgtcttgc ttgtggtttg 180
gtgttttagg cgggtgggga ggttgttgtg tagctgttgt atgtcatatt gttggtgttg 240
ctgccctgtg ctgtttgtcc ttggttattg tggttgttac cccgcctgtg tggaagtgtt 300
gtggcagggc gggaatttaa gtgggagagt tgtgggaccc gtggttgttg ttacgttgct 360
gcttttgtcg tgggcggtgg cggcgcgctc gataattaga attggatacg gagtgtataa 420
tacttctagt aaatggggac ctagtgcctg acttcccga atagggatct atgcgaagtc 480
cttaggatag tctttgataa gtttaacgcc cagcacccta aaattataca cgattagacg 540
cataacgact cctccaggaa agataaagaa tctcacatat agaacgggac cccatacacg 600
tcggatagga aacaagagaa ctaattttng ttaaaaagac tt 642

```

<210> 750

<211> 639

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(639)

<223> n=A,T,C or G

<400> 750

```

tttgtggcgg tgggtgtctca tttgggtgga tttttgggtc gtaggtaacc tgggtatngag 60
gtatagatgc cgattggtcc cgacgagcgt cagcataaat tcggtagttt cgcccttttt 120
agaaggcgct agtactcgga acttcacttc atctcggtag ttacttttgg cgtatatagc 180
cttctccctc gaagactagc cgtcacattc gttccctagg aatcgtttct gccctaaga 240
atccgagagc gagatcccga aactagagga accttagaag agtcgtattt ccacaaggac 300
cccacagtca ttccgggaaa atccctagga ccatacggtt aggattcccc cggaaccggg 360
agcaaagctc atgatttccc acaccgcgag agcgccata accctatccc atttcttcgg 420

```

275

```

gttatcgagg atattacgat caagccgaga gaaccgctag aaccgctttc ttcgctttct 480
cacggaacct ataagtagaa agagaaactc aggtcttaag ggggcgcttc ggctaacgaa 540
acttctactt acgaagagag tatctagaca ttaagtcata aaaatccact acgcacctcg 600
tgtacgatat catcgggagc ggttcataga cgggtgccg 639

```

```

<210> 751
<211> 637
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(637)
<223> n=A,T,C or G

```

```

<400> 751
cttttgtggc ggnggtgtct catttggtg gatttttggg tcgtaggnaa cctggtatng 60
aggcagctct gagccccccc ccccccccc cccccnccc ccccccccta ggnggttggg 120
aanacggtgg atacctaaat cgagtgngtt cattaaaagt agttgattac nccctaaaat 180
aanaanaggg cttcgtcggg anaaatcggg aagganaagt cttnttggca tcataanaat 240
actggctcgg gtcctaanaat ntttaaggng gtcnccgagg gtnttcatac cgataanaaa 300
cgttttctta tcggcaacgg gcttacctga gggnggactt ctncgngngc ggngattnan 360
acgaanacgt agaggattnc cgn tacttnt tganatcacn cgtatcatac ttgtaagcat 420
aattntcctg aaaagtgtta taanaatacg cncgcataatt cgctttttcg tcctagggat 480
gcttaaatgg cgatactgct atagcgggtg agcgttggtt ctcgagnaana aaagcgtgtc 540
ctaatacgctc taaggnttta agnccgttgg tttaaaaata nccttagaaa cctcgagggcg 600
gatactgggtt tntttttaac gaaacaaagc accccnn 637

```

```

<210> 752
<211> 644
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(644)
<223> n=A,T,C or G

```

```

<400> 752
tntgtggcgg tgggtgtcat ttgggtggat ttttgggtcg taggaacctg gtatgaggtc 60
ttgcgagttg ttggtgtgtc ctgtcgttcg gtggttcctt tttgagttga gtttgcctt 120
tgagggtgtt agctgctgtt cgtttgtgtt cgtgtagtgc tttgggttga gaggggttatg 180
gtgggtggtta cgggtgtattg tcgcccgtgg tcgcgggggtt ggggtgtgtc tcggttttgt 240
ggttcatagt agtcttctgc gttcgggtgtt gcgggttttg gtgagtagtt tcgttcttgg 300
atgtcccat gacccgccat aatctaagta agggttagta gaaacctct cccgatagac 360
acaaccgtcg tccactaaag acctcgcctc tgatttttaa aaggaccgga aaaacatccc 420
ttcaacggaa aaaacggaaa aaaagtcagc gaattcaaag aagccacggg agagaaaaaa 480
gaactaaagt tagtccgtca ttatatgtct cctcggagga ggaagcggcg gtggcgga 540
atgaggcggt aagaaagacg acctctatcg gcggcttang ccctaaaagg gcgatacctt 600
acgggatgat aaggacccta ggacgcctcc ttctcggatc gtcc 644

```

```

<210> 753
<211> 635
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature

```

276

<222> (1)...(635)

<223> n=A,T,C or G

<400> 753

```

ctttgtggcg gtggtgctca tttgggtgga tttttgggtc gtaggaacct ggtatgaggg 60
aatcagctcg accccccccc cccccccct ccgaagcaga gccaaccca aagtcaccg 120
actaccgag taaactctcg gagggtagaa taagaaggag taggtcctag ccaatagaag 180
tagttccgag ccgttaggac agcggacgga acattnaaga aagagcctat attagggagg 240
aagtaacgtt cctctttcgg agctctttaa ggggtagtcc cagaacaagg gaagaggacc 300
cgtcggctat tgcccgctga tacgggctct cacggngagc ctaggttcga ggatagggcc 360
gctcgtaaaa ttatacgggt tccgagaaac gcttccgtag accgggtcct aaatcgctcg 420
gagtattngg agagggatcc ttcggaccct agggacagag agaggagAAC ggaggttaca 480
ggaggagAAC gnttcctcnc tagttttctt tangtcgaaa aatttcttac cgataggggt 540
cctagggtcg gngaatttac ggttcgaaaa acggtagtnc ctaanggntg ntattngggg 600
tagtatcggg tcgtttacaa ntgcgtcgtc ttntg 635

```

<210> 754

<211> 721

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(721)

<223> n=A,T,C or G

<400> 754

```

accggattng ttncctgagcg cgtgactgct aataaaaaag atggantgcc atcttttttt 60
ttnccttgct ttatatatcc agcagcaaaa caaaattggt ctgcnggggt ataaaatttg 120
gcttgtagt cntgtacaca actcaggagt gtgacacagc taccagcttt cctcctaact 180
ctcaagggaa gaaaattcaa gttctgtcta ggctcactct gtaaagtggg aaacttgctg 240
gttttgtagg ctttttttcc cttcttttcc ctctctcagc ttctccctgc ttctcagaan 300
atggagttgt gatgcctgca acttaccaaa tttatctatg aatcagattc cagtgggaga 360
cccctaaagc agaggggagaa taaggagtcc tccccatgat ggaaaatatc caaagacaag 420
gtttcatgga gcaaaagaatt ctggctagat ttggtttgta agtggatccc tccccactgc 480
gtgtacactt tatctgtctc tttgcttctt cccacacctc ttcccgagct ctctctctgt 540
ctctctcttg ntccctgac ctttttttct tcccantgca taactttttt tttccctttt 600
ttaatcttct atantcttaa ncctaccaan gggccctcnt gannaatttn tcaccctga 660
ataggggatt ctntangccc tgagaatttc nttatcanaa aaatattttt ttaaagcatt 720
a 721

```

<210> 755

<211> 721

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(721)

<223> n=A,T,C or G

<400> 755

```

accggattng ttncctgagcg cgtgactgct aataaaaaag atggantgcc atcttttttt 60
ttnccttgct ttatatatcc agcagcaaaa caaaattggt ctgcnggggt ataaaatttg 120
gcttgtagt cntgtacaca actcaggagt gtgacacagc taccagcttt cctcctaact 180
ctcaagggaa gaaaattcaa gttctgtcta ggctcactct gtaaagtggg aaacttgctg 240
gttttgtagg ctttttttcc cttcttttcc ctctctcagc ttctccctgc ttctcagaan 300
atggagttgt gatgcctgca acttaccaaa tttatctatg aatcagattc cagtgggaga 360

```

277

```

cccctaaagc agagggagaa taaggagttc tccccatgat ggaaaatata caaagacaag 420
gtttcatgga gcaaagaatt ctggctagat ttggtttgta agtggatccc tccccactgc 480
gtgtacactt tatctgtctc ttgtcttctt cccaccctc tttcccagct ctctctctgt 540
ctctctcttg ntcccctgac ccttttttct tcccantgca tacttttttn tttccctttt 600
ttaatcttct atantcttaa ncctaccaan gggccctcnt gannaatttn tcaccctga 660
ataggggatt ctntangccc tgagaatttc nttatcanaa aaatattttt ttaaagcatt 720
a 721

```

<210> 756

<211> 873

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(873)

<223> n=A,T,C or G

<400> 756

```

ggaagaatac agtaagtttg caaattaaaa tttctctatt tttctgttat ttattcattt 60
ggaaactgtc agcctgtctc tttcactttg ggcaagttaa agcaaagacg tccagtccta 120
tcagcaatta ggctgaaagt caacgccaaag ctggcgggca agggctgggc tgagtagagg 180
ttccctaggc aggcaagaga gagactccca ctcgatactc ccagctcggc aactgcctga 240
atgccaatga gcactcatta taaccgcgcc tattttatag gatttaattt tacacttcag 300
gcttaatcag tctgaaagt aaactgacag tggttaagtt cggaatcaat gacatttagg 360
ctttatgact ttgtagctga atatctatgg gctatatttc cattctaaca gtgatatcct 420
gttccagaat ctcatctctt ggtgatggca ctttctagtg gagcagtcac ggtaacagtc 480
cacaccatt accatgtggg tgctttacag catactgacg gaaggactga ggagccaccg 540
gagcaggagt tcctctcagg gaggacgctg acacttccac agctgcctan gtatgggcac 600
ctgatgcaa cgaanaaccc aaagcgctct cccttcaga tggaagctgc cccacactgg 660
gctgacagca atgtgctgc ctctggctca aatcccggaa tcgcacancn cctancgggg 720
gcgtttanag atcctcnggg ccagctaccg accacttttg acaagggnct taggagcgat 780
aactagnctg gcgcgttaca cncggatgga acgtcttgga cttgagacct cttgggggan 840
atggcncccc caaataantt gggaaaantn ggg 873

```

<210> 757

<211> 782

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(782)

<223> n=A,T,C or G

<400> 757

```

ggccccctga gggatactct agagcgcccg ccgactagt agctcgtcga cgatatcccg 60
ggattfgaga ccaggagaca gctccagatg ctgtcagccc agtgctgggg gcaggcttcc 120
atctgtgaag tggagaggcg ctttgggctt ctctcgttggc atcaggtgcc catacctagg 180
gcagctgtgg aagtgtcagc gtccctcccg agaggaaact ctgctccggg ggctccctag 240
tccttccgctc agtatgctgt aaagcaccca catggtaatg ggtgnggact ggtaccatga 300
ctgntccctt aaaaggtggc cttccnaag aaaggagaat tcttggaacna gggatttcac 360
ttgnttagaa atgggaaaaa ttaccattta gaattttcgn ttccaaggcn tnaagncccta 420
aaaggccttt gattcccga ccttaaccct gggcagttaa cctttcaaac gggataaacc 480
ctgaggggga aaatnaaatc ctttaaaaaa ggggggggtt naaggagggc tctttggcct 540
tcaggcantt gccaacctgg gaaattcana ggggaagtnt ttttttttgc ctgectaggg 600
aacctttact taaacnaacc cttgnccccc catttggggt tgactttcan cctaattgct 660
gaaaggaccg ggccgntttt gntttccttt gncccaaagg naaanaaacg ggtgccantt 720

```

278

cccangggat tanttcccga aaatttggnn aatttttntt tгнаactttt tgggtttttt 780
cc 782

<210> 758
<211> 647
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(647)
<223> n=A,T,C or G

<400> 758
ntttgtggcg gtggtgtctc atttgggtgg actttttggg tcgtaggaac ctggtatnga 60
gggaagagcg ccgctcggtcc gagtacagta tggagtagta tagtcttcgc gccttctcgg 120
gcggcggggc tattctctcc aaaggcagag gtccctagtc gacctcgctc ccctagggtta 180
ggaacagccg tcgaatattt taggttcgtc gaggttttct tccgagctct acgcctaagt 240
agctccgcga gcaaagtatc ggtcattttc ccctatccat cactccccta agtacgcctc 300
attattccgg aaggcaagag gccagcattc ctcccttagag tagagggtag gtacctccgt 360
cgcgtgccgc gaaagggcag agcttcgtgt ctccctccg cagcagctta acggtctacg 420
taggcgttct cgatcttttc acgggaatcg gggtcggga gggcgccgga aaacgctcgac 480
gtctcggtea ccgtcaccgc cccgaacaac tagcggcttt ccgctttcaa ctgaggaacc 540
ccgcacccct cattagcgt tacgaaatcg gggangtgat tgcgccaatt cgttagcctt 600
cgataattat tctctattag cggtcctatc tcgcgctttc gatttat 647

<210> 759
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(657)
<223> n=A,T,C or G

<400> 759
ctttgtggcg gtggtgtctc atttgggtgg actttttggg tcgtaggaac ctggtatnga 60
gggtctctata gaaagcctct tgtcttttaga tacgggcttt ctggtccttc gttctggaag 120
tgtagtagta ggtactgcgg gaaggcgaag agtcctttca aggacgattt acttaagttg 180
gcttattcta tagttccttc gggacataag gtccgtacga tctatactgc gtgggaagct 240
gataggtttg gacttaaggc gaataagaag gaggcggcgg aggtcgcgat taccgcagag 300
atattattta cggcgccgc gggtagccgc ggtcatgcgg aaattttctg aggttcttg 360
attcctaaga tcgctcccgt cgagtatact agcgacgaac gtaagagtgc cctcacaaga 420
accggtacaa actcaagaag aagttcccat taagcatcgt aagaaacggg aggacgagga 480
cggtaagaag taatcggaga aaggatccta gtngttacga agaagcatcg ttnagctact 540
ttgcgctacc gtttatattt agacgtgttc cgtccttctc cgtgtttana aaaaagggtt 600
attccgacgg gagacttagg cgaatggagg gttccgcggg tganaatcgg ancgggg 657

<210> 760
<211> 644
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(644)
<223> n=A,T,C or G

279

<400> 760

```

ctttgtggcg gtggtgtctc atttgggtgg acttttttggg tcgtaggaac ctggtatgna 60
ggaaaagaag taagcctcga agcctatctc cgaccgtatt tatttcgcag aagacggaac 120
tacggacgctc gttaaccccg agtagccccc gtaagaaagg actaaagcga atggaaaagt 180
cgggaattcc ggccggagggg cggcgattac tgaaaggagt aagagtaaga ctattgcgat 240
acttgaggcg ttccctctta aaaggcaccg gaaacactct attaaaaaac acccgaagaa 300
gaacaactca tgcgatcggc cgtgtgcagc cgtcaatagt aaagagagcc atgaaccatg 360
ccatccttag accaattagg atgaagaaga ggaggaagat gaggaccaa ccctaccac 420
tcggaaaacc ccgcacgagc ctccgaacaa aatccgggaa ttaaacggc ggccacttc 480
cgactctcg tagcgcgagc cgaatagaaa accggaaact acagctaaag ggtcctttcc 540
ggcctgttat ctaccaccc gcaatccgat cctccccccc cctcgtccaa aaaccctaac 600
ctctgcggca acattagagc agaaggagag ggcgatccct tgan 644

```

<210> 761

<211> 647

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(647)

<223> n=A,T,C or G

<400> 761

```

ctttgtggcg gtggtgtctc atttgggtgg acttttttggg tcgtaggaac ctggtatnga 60
ggcgggtact ctctgggata atcgggtataa gtgttgtaaa attgggggta agagaaagtt 120
tcattataag aagtggaagc acgagccggg gtgttttagtc gttaatatta agaccggttt 180
ttgttgtagt tatatagctt gcgcgtgggg aggcaataag aaacattgcg ttccgaggcc 240
ggatgcgggg aaccctcttc ggggtctaga gcgccgcac tgcaaaaataa ggactactga 300
cgccgctcat aacgtactca acaatgagtc ggccgtcatt aagatttcgg cgaagaaccg 360
tactgcgtct actgatagta tattgcattg atagcggcat gagctttatc acgtgtcggt 420
ttcgggttgt aagaaggag ttaagtcgat cttcgaggaa gaagagacc caaataaaaa 480
atgactcaaa aaaacctaga agaaacacga cgaaaggaaa aagaacgtta aaactagtag 540
ctcttcggan gtagtagcctt agtagggtaa gtcctccgtg cgtactgtcc taagggtttg 600
atagcgcggt tgaatagacg gtcacgcgtc agaaggtaaa aanccgg 647

```

<210> 762

<211> 628

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(628)

<223> n=A,T,C or G

<400> 762

```

cattgtgttg gggtcactga gcccactttt ttccagattt tttgtaaaat tgtttcgcac 60
tgtgtccct ttattcgctt gtattaatat ttgcgtagtg gattaaacaa atacttggtg 120
ttgactgtca gtcttagagg actgactaga agtagttttc atttggggct caggaaatac 180
ctactttata tttctagcta attaggaaag tcatttttca gttagggttg tgttttggtt 240
caggcactcg ctagctagat gacctaacat gctacttaat ttctgagtgt ttgtgtccat 300
ccctgtagga ttgttgccgg gttaaataaa attgtgtata tttgtaaagc atttacctca 360
gtgccagagc tgtgacagag tagattatta ggcttgctct tatttctgtg attaaattta 420
gtgtcagatt agcaacctat agctacttct aaagctgctg ctgctttctt tgtttagggt 480
taggaagaaa catgctggac agtttgccaa atgagagtta catgatgtgg cttgtgggaa 540
cattctaact tggaacttgc ccatttccag gactttngng ttcanagatt tttggggata 600

```

280

gatgtaaggg ttaaaaaaaaa cngaaaac

628..

<210> 763

<211> 147

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(147)

<223> n=A,T,C or G

<400> 763

cattgtgttg gggcagagat aaataattcc tctgaaaagt gttttattgg aatttcaaat 60
 gaaaagctaa ctggataact tacagcatgt ttctgccaat aatctcttan aacaggcctc 120
 ttttttttat gcacaccacc ttcnnggc 147

<210> 764

<211> 146

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(146)

<223> n=A,T,C or G

<400> 764

cattgtgttg ggtatgtttt ttgaaggcag gtggacagga tttgctgatg ggtaaatggc 60
 agagttaggg ggactgttag aacagagaaa.ganatcatgg ggttgggttt gagtctgatg 120
 nnnaactggt gccgmntgct cagtat 146

<210> 765

<211> 129

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(129)

<223> n=A,T,C or G

<400> 765

tncncgattc gntnctagcg tntacactna tgtcttggtta ccgagctcgg atccactagt 60
 ccagtgtggg nggaattcca ttgtgttggtg gcaggaggng ctttgngtac ngtgcggctg 120
 nagaggcgg 129

<210> 766

<211> 175

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(175)

<223> n=A,T,C or G

<400> 766

281

```

cattgtgttg ggcctagtcc gaatactttt agtaacttca gacagatctc ctcactctctt 60
tctggggcctt ggnttttctc ctttgtanaa tgatgccttt ctgtggtttt gtcattttcta 120
acattctgtg ngtgatgagg tgtatattcg angantctta tcnccanagt actct 175

```

<210> 767

<211> 602

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(602)

<223> n=A,T,C or G

<400> 767

```

nnnttttaaaa nctgtntctcc ccgcggtggc ggccgctcta gaactagtgg atcctttcca 60
cctgggtttgt tttcagtggt taatcctatt agtatcagca ggatataggt caggatatca 120
ggtgcagaac ctgtggaatc agccaatttg gcttgcctcat ttactttaat aagggtcccat 180
aatgagtgag agtacaaagt tcaagccctg ttgaggggtct gcattaaact ctcagaagta 240
tttagagtggt gccaggagcc gcgaaggctt gggtcggttg gtggcgggaa ctgtattaga 300
gtgctaggca cggcgcgaca aagtctgtcc aacccaaaac ggtgctgagg cgttgggtgt 360
gagctccagt actcagaaaa gcatctcagc aggtactcaa cagatcctca ggggcttggg 420
ggcccagcac tggcagtgag ggcatgaaag acataaaagg gcactacctg tgggtatttt 480
ctgttctcca aggaggaagt agcaaaaatt aggacgctgg aatatcctat gttgtagcaa 540
tcccagaaca actgatgctc aacaaaatcc acacaaaaca aattttttaa aatttaattct 600
ta 602

```

<210> 768

<211> 671

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(671)

<223> n=A,T,C or G

<400> 768

```

tccaccgagg tggcgggcgc tctagactag tggatccact agtccagtgt ggggtgggaat 60
tcgcggcncg cgtcgacaaa aatactgcta aagtaatatt tttatagatg actatttgcc 120
ttggggccag gaaaagcagc tggagttatt cacttagtac cttttttaca tactaacttt 180
gcctttttcca tgcttgcttg atgcggcttg cagcactgaa gaacagtttc aattgctagc 240
caaccagaga gcatgatcaa accaaaacag ttccctgttt caggaaaaac aggttttagg 300
taactgaagg gttaccagtt actgattcca caatcttctc tgtaaaanatt ttctgcctat 360
tatgcagact gggcggtctt aaanntggta aaactatnaa ataccatac aatattttta 420
nggggccccn ttatnaagct tttcaggcct tcccctttcc atagcattgg tgggatacaa 480
gaaaccttta aacagcaacn agctatcnag gcccaaaagg aaagtaattn tgatttttta 540
nagattccgn aacgaaaaaa tggctgggtt caaatacnac cttcttttta aaatggnttc 600
cttattaaac ntnttttttt tttaatttta ccccatggtc ntgatnttng ngcttccgcc 660
canaaaatng n 671

```

<210> 769

<211> 877

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

282

<222> (1)...(877)

<223> n=A,T,C or G

<400> 769

```

aaagctggag ctccccgcgg tggcggccgc tctagaacta gtggatccac tagtccanng 60
ngggggaatt cgcgccgcgg tgcacctcta tacctttgnt catgcagctt cctctgactg 120
ggtttggtct tcaactggct aaccctctt ttacttaagc acaccttgaa cattccctcc 180
ttccccattt ccccgagng cccctaattg acatacttct gaataacaca ggtggtattc 240
cttcttgtt ggaacctcct ggaggaagag acagatgatt aacaaatcct tccatcaacc 300
cctttgacca tgacatcaac agtgctccaa attatggggt accgtattag cctatgtcta 360
tcttgatcag aatccttacc tcggtgtatt gaaattatct atttcgtgcc tgcctcttta 420
aagtcagggt ttgccttacc tattgtctaa caccatgcag taggtaacat gcagtaggaa 480
acatggcatt aaattatttg ggttcaaadc ccagttatgg tgtgtaaag cctaccaggc 540
cgtgaggcac ctgctaagca ggttgacgc atcatttgaa ttcacaccac ccttttgcaa 600
tagaacagat aggcaacaga ggctcatttg ggctaaagga tttgatggag gggaagtgcc 660
aggattccca ccaaggcctc anggccagg tccanggacc atgtctgttg tgacaactgg 720
agtgcatttc atatcccctn ctctgngggg naagggtccct cncgnggaga acnnttaaaa 780
caatcatntc tngggggntt aatgcttctt nccccagtggt ggtncactgc ngccacagat 840
cccancact agtcccangt ctgtcatgaa ccanc 877

```

<210> 770

<211> 874

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(874)

<223> n=A,T,C or G

<400> 770

```

ctggnctccc cgcggtggcg gccgctctag aactagtggg tccactagtc cagtgtgggtg 60
gaattcgcg cgcgctcgac cttttcaaag gttaacttat ttaattatca canngcaac 120
ccgatgagta ggtaacagta ttttactgat aggtaatcta aagaaggagg ctaaaataaat 180
tgcccaattt cgaacagtga gaggaagaat taggattgaa acacatatag tggcttcaga 240
atctgtaacc ctcacgatgc cactactact totttcagaa taccctttgc ctatctattc 300
tgttcctatg tcatcaaatt atacttactt taaaaagtat ttgtctttat tattttttaa 360
aaaacacagg gaagtatttc tgatcagggg cagtattggg tctgaaagac aagccagtgt 420
ttttgagggt ttctcccttg ccagtttttc tatgctgggt tattcaagtc ctaagaattg 480
tgtagctatt acagaaccgc tttagcaaat gtgttccatt aatcaagggt atttataaca 540
aaatttcac caagtttgga gtgctctgaa aacatagcca aaatgttcgc aggtctacc 600
cctctcgtgt gtcccttttt tttagctatt tcagaagcac actggtgcaa tattttacga 660
aatgagtttc ttccctttac ctctgcatcc tctaagaaaa aatcattgnt gttttatgaa 720
natgaanac ctgctatttc atatcttgat tggagctgct taattaaatg accatttttna 780
aatttgtttt gattccnngc aaaaaaagtt tnttnttggg tgtagggggc tcnnaaagnc 840
caaaaccccc caaaattttt nnttggaac ccna 874

```

<210> 771

<211> 156

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(156)

<223> n=A,T,C or G

<400> 771

283

```

ttaaaaaanct ggncctccccg cgggtggcggc cgctctagaa ctagtggatc cactagtcca 60
gtgtgggtgga attcgcggcc gcgtcgaccg cgagcgggtcg cccttttttt tttttttttn 120
ngttttttttg aanaattcat tgggtattta ttattc 156

```

<210> 772

<211> 586

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(586)

<223> n=A,T,C or G

<400> 772

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<210> 773

<211> 2983

<212> DNA

<213> Homo sapiens

<400> 773

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<210> 774

<211> 3064

<212> DNA

<213> Homo sapiens

<400> 774

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285

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<210> 775

<211> 684

<212> PRT

<213> Homo sapiens

<400> 775

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Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
                    35                      40                      45
Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
                    50                      55                      60
Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
                    65                      70                      75                      80
Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
                    85                      90                      95
Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
                    100                      105                      110
Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
                    115                      120                      125
Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
                    130                      135                      140
Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
                    145                      150                      155                      160
Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
                    165                      170                      175
Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
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Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp

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286

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	245	250
Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala		255
	260	265
Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser		270
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Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val		285
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Pro Asp Leu Pro Lys Gly Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr		335
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Pro Gln Glu Arg Ser Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu		350
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Thr Ala Ile Arg Lys Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe		365
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Val Phe Ser Glu Val Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met		380
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	405	410
Ile Gly Lys Asn Ile Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg		415
	420	425
Asp Ile Thr Tyr Glu Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg		430
	435	440
Gln Val Met Asp His Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His		445
	450	455
Arg Arg Pro Val Lys Glu Asn Phe Leu His Met Ser Val Gln Ser Asp		460
465	470	475
Asp Val Leu Leu Gly Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg		480
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Lys Thr Ala Ala Leu Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu		495
	500	505
Gln Leu Tyr Thr Gly Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys		510
	515	520
Thr Ser Gln Ile Gln Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp		525
	530	535
Ser Lys Thr Tyr Ile Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val		540
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Ile Arg Gly Phe Ile Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met		560
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Ala Ser Glu Val Phe Thr Ser Phe Gln Tyr Pro Glu Phe Ser Ile Glu		575
	580	585
Leu Pro Asn Thr Gly Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile		590
	595	600
Phe Lys Asn Thr Leu Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu		605
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Glu Ser Leu Gly Ile Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val		620
625	630	635
Gln Pro Gly Glu Thr Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys		640
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Thr Gly Pro Lys Lys Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys		655

287

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 <210> 776
 <211> 679
 <212> PRT
 <213> Homo sapiens

 <400> 776
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 35 40 45
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 Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
 65 70 75 80
 Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
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 Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
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 Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
 115 120 125
 Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
 130 135 140
 Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
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 Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
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 Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp
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 Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys
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 Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly
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 Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val
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 Asp Thr Tyr Val Asn Glu Asn Gly Glu Lys Ile Thr Ser Met Thr His
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 Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg
 325 330 335
 Pro Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr Pro Gln Glu Arg Ser
 340 345 350
 Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu Thr Ala Ile Arg Lys
 355 360 365
 Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe Val Phe Ser Glu Val
 370 375 380

288

Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met Val Asn Gly Gln Glu
 385 390 395 400
 Glu Leu His Val Ile Ser Met Glu Thr Thr Ser Ile Gly Lys Asn Ile
 405 410 415
 Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg Asp Ile Thr Tyr Glu
 420 425 430
 Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg Gln Val Met Asp His
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 Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His Arg Gln Pro Val Lys
 450 455 460
 Glu Asn Phe Leu His Met Ser Val Gln Ser Asp Asp Val Leu Leu Gly
 465 470 475 480
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 Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu Gln Leu Tyr Thr Gly
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 Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys Thr Ser Gln Ile Gln
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 Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp Ser Lys Thr Tyr Ile
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 Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val Ile Arg Gly Phe Ile
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 Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met Ala Ser Glu Val Phe
 565 570 575
 Thr Ser Asn Gln Tyr Pro Glu Phe Ser Ile Glu Leu Pro Asn Thr Gly
 580 585 590
 Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile Phe Lys Asn Thr Leu
 595 600 605
 Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu Glu Ser Leu Gly Ile
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 Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys Thr Gly Pro Lys Lys
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<210> 777

<211> 5668

<212> DNA

<213> Homo sapiens

<400> 777

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<211> 1095

<212> PRT

<213> Homo sapiens

<400> 778

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Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
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Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
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292

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<211> 3639

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<213> Homo sapiens

<400> 779

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<211> 1095

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<213> Homo sapiens

<220>

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Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp															
			435				440						445		
Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe															
			450			455						460			
Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr															
465					470					475					480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val															
			485						490						495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu															
			500					505						510	
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys															
			515				520						525		
Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val															
			530			535				540					
Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile															
545					550					555					560
Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg															
			565					570						575	
Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu															
			580					585					590		
Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu															
			595				600						605		
Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr															
			610			615							620		
Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu															
625					630					635					640
Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp															
			645						650					655	
Gln His Phe Ile Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln															
			660					665						670	
Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu															
			675				680						685		
Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg															
			690			695				700					
Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala															
705					710					715					720
Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr															
			725						730					735	
Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His															
			740					745					750		
Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val															
			755				760						765		
Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr															

770		775		780
Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe				
785		790		795
Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu				
	805		810	815
Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu				
	820		825	830
Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile				
	835		840	845
Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu				
	850		855	860
Phe Ala Xaa Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu				
865		870		875
Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr				
	885		890	895
Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly				
	900		905	910
Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys				
	915		920	925
Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu				
	930		935	940
Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile				
945		950		955
Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr				
	965		970	975
Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu				
	980		985	990
Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val				
	995		1000	1005
Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys				
1010		1015		1020
Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp				
1025		1030		1035
Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val				
	1045		1050	1055
Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg				
	1060		1065	1070
Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys				
	1075		1080	1085
Glu Ile Ala Asn Lys Ile Lys				
1090		1095		

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 Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser
 5 10 15

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 <212> DNA
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<400> 782

297

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<211> 42
<212> DNA
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ttccagaact cctacaccat cgggctgggc ctgcacagtc tt 42

<210> 788
<211> 45
<212> DNA
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<400> 788
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<210> 789
<211> 45
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catccgcagt ggggtgctgtc agccgcacac tgtttccaga actcc 45

298

<210> 790
<211> 45
<212> DNA
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<210> 791
<211> 45
<212> DNA
<213> Homo sapiens

<400> 791
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<210> 792
<211> 45
<212> DNA
<213> Homo sapiens

<400> 792
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<210> 793
<211> 51
<212> DNA
<213> Homo sapiens

<400> 793
tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc g 51

<210> 794
<211> 45
<212> DNA
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<210> 795
<211> 45
<212> DNA
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<210> 796
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299

<211> 45

<212> DNA

<213> Homo sapiens

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45

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<211> 45

<212> DNA

<213> Homo sapiens

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45

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<211> 15

<212> PRT

<213> Homo sapiens

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5 10 15

<210> 800

<211> 15

<212> PRT

<213> Homo sapiens

<400> 800

Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu
5 10 15

<210> 801

<211> 15

<212> PRT

<213> Homo sapiens

<400> 801

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
5 10 15

<210> 802

<211> 15

<212> PRT

<213> Homo sapiens

<400> 802

Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu
5 10 15

<210> 803

<211> 14

<212> PRT

300

<213> Homo sapiens

<400> 803

Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
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<210> 804

<211> 15

<212> PRT

<213> Homo sapiens

<400> 804

Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
5 10 15

<210> 805

<211> 15

<212> PRT

<213> Homo sapiens

<400> 805

His Pro Gln Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser
5 10 15

<210> 806

<211> 15

<212> PRT

<213> Homo sapiens

<400> 806

Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His
5 10 15

<210> 807

<211> 15

<212> PRT

<213> Homo sapiens

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Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
5 10 15

<210> 808

<211> 15

<212> PRT

<213> Homo sapiens

<400> 808

Ala Leu Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val
5 10 15

<210> 809

301

<211> 17
<212> PRT
<213> Homo sapiens

<400> 809
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5 10 15

Ser

<210> 810
<211> 15
<212> PRT
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<400> 810
Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu
5 10 15

<210> 811
<211> 15
<212> PRT
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<400> 811
Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser
5 10 15

<210> 812
<211> 15
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<400> 812
Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser
5 10 15

<210> 813
<211> 15
<212> PRT
<213> Homo sapiens

<400> 813
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
5 10 15

<210> 814
<211> 15
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<213> Homo sapiens

<400> 814

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<211> 652
<212> PRT
<213> Homo sapiens
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Ser	Ser	Ala	Ser	Arg	Ser	Thr	Asp	Leu 25	Ser	Tyr	Ser	Glu	Ser 30	Asp	Leu
Val	Asn	Phe 35	Ile	Gln	Ala	Asn	Phe 40	Lys	Lys	Arg	Glu	Cys 45	Val	Phe	Phe
Thr	Lys 50	Asp	Ser	Lys	Ala	Thr 55	Glu	Asn	Val	Cys	Lys 60	Cys	Gly	Tyr	Ala
Gln 65	Ser	Gln	His	Met 70	Glu	Gly	Thr	Gln	Ile	Asn 75	Gln	Ser	Glu	Lys	Trp 80
Asn	Tyr	Lys	Lys	His 85	Thr	Lys	Glu	Phe	Pro 90	Thr	Asp	Ala	Phe	Gly 95	Asp
Ile	Gln	Phe	Glu 100	Thr	Leu	Gly	Lys	Lys 105	Gly	Lys	Tyr	Ile	Arg 110	Leu	Ser
Cys	Asp	Thr 115	Asp	Ala	Glu	Ile	Leu 120	Tyr	Glu	Leu	Leu 125	Thr	Gln	His	Trp
His	Leu 130	Lys	Thr	Pro	Asn	Leu 135	Val	Ile	Ser	Val	Thr 140	Gly	Gly	Ala	Lys
Asn 145	Phe	Ala	Leu	Lys 150	Pro	Arg	Met	Arg	Lys	Ile 155	Phe	Ser	Arg	Leu	Ile 160
Tyr	Ile	Ala	Gln 165	Ser	Lys	Gly	Ala	Trp	Ile 170	Leu	Thr	Gly	Gly	Thr 175	His
Tyr	Gly	Leu 180	Met	Lys	Tyr	Ile	Gly	Glu 185	Val	Val	Arg	Asp	Asn 190	Thr	Ile
Ser	Arg	Ser 195	Ser	Glu	Glu	Asn 200	Ile	Val	Ala	Ile	Gly 205	Ile	Ala	Ala	Trp
Gly	Met 210	Val	Ser	Asn	Arg	Asp 215	Thr	Leu	Ile	Arg	Asn 220	Cys	Asp	Ala	Glu
Gly 225	Tyr	Phe	Leu	Ala 230	Gln	Tyr	Leu	Met	Asp	Asp 235	Phe	Thr	Arg	Asp	Pro 240
Leu	Tyr	Ile	Leu	Asp 245	Asn	Asn	His	Thr	His 250	Leu	Leu	Leu	Val	Asp 255	Asn
Gly	Cys	His 260	Gly	His	Pro	Thr	Val	Glu 265	Ala	Lys	Leu	Arg	Asn 270	Gln	Leu
Glu	Lys	Tyr 275	Ile	Ser	Glu	Arg	Thr 280	Ile	Gln	Asp	Ser	Asn 285	Tyr	Gly	Gly
Lys	Ile 290	Pro	Ile	Val	Cys	Phe 295	Ala	Gln	Gly	Gly 300	Gly	Lys	Glu	Thr	Leu
Lys 305	Ala	Ile	Asn	Thr 310	Ser	Ile	Lys	Asn	Lys	Ile 315	Pro	Cys	Val	Val	Val 320
Glu	Gly	Ser	Gly 325	Gln	Ile	Ala	Asp	Val	Ile 330	Ala	Ser	Leu	Val	Glu 335	Val
Glu	Asp	Ala	Leu	Thr	Ser	Ser	Ala	Val	Lys	Glu	Lys	Leu	Val	Arg	Phe

304

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      340      345      350
Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp
      355      360      365
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
      370      375      380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
385      390      395      400
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
      405      410      415
Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
      420      425      430
Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
      435      440      445
Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
      450      455      460
Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
465      470      475      480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
      485      490      495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
      500      505      510
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
      515      520      525
Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
      530      535      540
Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
545      550      555      560
Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
      565      570      575
Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
      580      585      590
Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
      595      600      605
Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
      610      615      620
Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
625      630      635      640
Ala Trp Gly Gly Leu Glu His His His His His His
      645      650

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<210> 819

<211> 132

<212> PRT

<213> Homo sapien

<400> 819

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Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
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      20      25      30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
      35      40      45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
      50      55      60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65      70      75      80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala

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305

				85					90					95					
Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser	Val	Asn	Trp				
			100					105						110					
Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu				
		115					120					125							
Gly	Pro	Pro	Ala																
	130																		

<210> 820
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 820
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<210> 821
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 821
 gggctcgagt caggagtttg agaccagcct ggc 33

<210> 822
 <211> 675
 <212> DNA
 <213> Homo sapiens

<400> 822
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 accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
 ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
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 gcgcttaacg ggcacatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
 ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt catgatccgg 420
 gagaaatttg cccactgcac cgtgctaacc attgcacaca gattgaacac cattattgac 480
 agcgacaaga taatggtttt agattcagga agactgaaag aatatgatga gccgtatggt 540
 ttgctgcaaa ataaagagag cctattttac aagatgggtg aacaactggg caaggcagaa 600
 gccgctgccc tcaactgaaac agcaaaacag agatgggggtt tcaccatggt ggccaggctg 660
 gtctcaaact cctga 675

<210> 823
 <211> 291
 <212> DNA
 <213> Homo sapiens

306

<400> 823

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gagccgtatg ttttgcgtgca aaataaagag agcctatttt acaagatggt gcaacaactg 180
ggcaaggcag aagccgctgc cctcactgaa acagcaaaac agagatgggg tttcaccatg 240
ttggccaggc tgggtctcaa ctcctctgag caccaccacc accaccactg a 291

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<210> 824

<211> 1074

<212> DNA

<213> Homo sapiens

<400> 824

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gtgcatgtgc aggattttac tgctttttgg gataaggcat cagagacccc aactctacaa 180
ggcctttcct ttactgtcag acctggcgaa ttgttagctg tggtcggccc cgtggggagca 240
gggaagtcac cactgttaag tgccgtgctc ggggaattgg cccaagtca cgggctgggc 300
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aggagtaata ttttatttgg gaagaaatac gaaaaggaaac gatatgaaaa agtcataaaag 420
gcttgtgctc tgaaaaagga tttacagctg ttggaggatg gtgatctgac tgtgatagga 480
gatcggggaa ccacgctgag tggagggcag aaagcacggg taaaccttgc aagagcagtg 540
tatcaagatg ctgacatcta tctcctggac gatcctctca gtgcagtaga tgcggaagtt 600
agcagacact tggtcgaact gtgtatttgc caaattttgc atgagaagat cacaatttta 660
gtgactcatc agttgcagta cctcaaagct gcaagtcaga ttctgatatt gaaagatggg 720
aaaatggtgc agaaggggac ttacactgag ttccataaat ctggatataga ttttggctcc 780
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aaagatgggt ctctggagag ccaagataca gagaatgtcc cagttacact atcagaggag 960
aaccgttctg aaggaaaagt tgggttttcag gcctataaga attacttcag agctgggtgct 1020
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<210> 825

<211> 224

<212> PRT

<213> Homo sapiens

<400> 825

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Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
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Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
      20      25      30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
      35      40      45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
      50      55      60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
      65      70      75      80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
      85      90      95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
      100      105      110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
      115      120      125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Ile Arg Glu Lys Phe Ala
      130      135      140
His Cys Thr Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp

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307

145					150					155					160
Ser	Asp	Lys	Ile	Met	Val	Leu	Asp	Ser	Gly	Arg	Leu	Lys	Glu	Tyr	Asp
				165					170					175	
Glu	Pro	Tyr	Val	Leu	Leu	Gln	Asn	Lys	Glu	Ser	Leu	Phe	Tyr	Lys	Met
			180					185					190		
Val	Gln	Gln	Leu	Gly	Lys	Ala	Glu	Ala	Ala	Ala	Leu	Thr	Glu	Thr	Ala
		195					200					205			
Lys	Gln	Arg	Trp	Gly	Phe	Thr	Met	Leu	Ala	Arg	Leu	Val	Ser	Asn	Ser
	210					215					220				

<210> 826

<211> 357

<212> PRT

<213> Homo sapiens

<400> 826

Met	Ser	Ala	Ile	Glu	Arg	Val	Ser	Glu	Ala	Ile	Val	Ser	Ile	Arg	Arg
				5					10					15	
Ile	Gln	Thr	Phe	Leu	Leu	Leu	Asp	Glu	Ile	Ser	Gln	Arg	Asn	Arg	Gln
			20					25					30		
Leu	Pro	Ser	Asp	Gly	Lys	Lys	Met	Val	His	Val	Gln	Asp	Phe	Thr	Ala
		35					40					45			
Phe	Trp	Asp	Lys	Ala	Ser	Glu	Thr	Pro	Thr	Leu	Gln	Gly	Leu	Ser	Phe
	50					55					60				
Thr	Val	Arg	Pro	Gly	Glu	Leu	Leu	Ala	Val	Val	Gly	Pro	Val	Gly	Ala
	65				70					75					80
Gly	Lys	Ser	Ser	Leu	Leu	Ser	Ala	Val	Leu	Gly	Glu	Leu	Ala	Pro	Ser
			85						90					95	
His	Gly	Leu	Val	Ser	Val	His	Gly	Arg	Ile	Ala	Tyr	Val	Ser	Gln	Gln
		100						105					110		
Pro	Trp	Val	Phe	Ser	Gly	Thr	Leu	Arg	Ser	Asn	Ile	Leu	Phe	Gly	Lys
	115						120					125			
Lys	Tyr	Glu	Lys	Glu	Arg	Tyr	Glu	Lys	Val	Ile	Lys	Ala	Cys	Ala	Leu
	130					135					140				
Lys	Lys	Asp	Leu	Gln	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Thr	Val	Ile	Gly
	145				150					155				160	
Asp	Arg	Gly	Thr	Thr	Leu	Ser	Gly	Gly	Gln	Lys	Ala	Arg	Val	Asn	Leu
				165					170					175	
Ala	Arg	Ala	Val	Tyr	Gln	Asp	Ala	Asp	Ile	Tyr	Leu	Leu	Asp	Asp	Pro
		180						185					190		
Leu	Ser	Ala	Val	Asp	Ala	Glu	Val	Ser	Arg	His	Leu	Phe	Glu	Leu	Cys
	195						200					205			
Ile	Cys	Gln	Ile	Leu	His	Glu	Lys	Ile	Thr	Ile	Leu	Val	Thr	His	Gln
	210					215					220				
Leu	Gln	Tyr	Leu	Lys	Ala	Ala	Ser	Gln	Ile	Leu	Ile	Leu	Lys	Asp	Gly
	225				230					235				240	
Lys	Met	Val	Gln	Lys	Gly	Thr	Tyr	Thr	Glu	Phe	Leu	Lys	Ser	Gly	Ile
				245					250					255	
Asp	Phe	Gly	Ser	Leu	Leu	Lys	Lys	Asp	Asn	Glu	Glu	Ser	Glu	Gln	Pro
			260					265					270		
Pro	Val	Pro	Gly	Thr	Pro	Thr	Leu	Arg	Asn	Arg	Thr	Phe	Ser	Glu	Ser
	275						280					285			
Ser	Val	Trp	Ser	Gln	Gln	Ser	Ser	Arg	Pro	Ser	Leu	Lys	Asp	Gly	Ala
	290					295					300				
Leu	Glu	Ser	Gln	Asp	Thr	Glu	Asn	Val	Pro	Val	Thr	Leu	Ser	Glu	Glu
	305				310					315					320
Asn	Arg	Ser	Glu	Gly	Lys	Val	Gly	Phe	Gln	Ala	Tyr	Lys	Asn	Tyr	Phe

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          325          330          335
Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Glu His
          340          345          350
His His His His
          355

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<400> 827

<210> 828
<211> 35
<212> DNA
<213> Artificial Sequence

<400> 828
cgcccatggg gatccgggag aaatttgccc actgc

35

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<210> 829
<211> 35
<212> DNA
<213> Artificial Sequence
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<220>
<223> PCR primer

<400> 829
cgctctgagg gagtttgaga ccagcctggc caaca

35

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<210> 830
<211> 38
<212> DNA
<213> Artificial Sequence
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<220>
<223> PCR primer

<400> 830

309

gcatggacca tatgtcagcc attgagaggg tgtcagag

38

<210> 831

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 831

ccgctcgaga ataaggaaaa tgaagacaat ccag

34

<210> 832

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 832

gttgaattca tgcacgggcc ccaggtg

27

<210> 833

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 833

cccctcgagt cactatgggtc tgcctcttga

30

<210> 834

<211> 915

<212> DNA

<213> Homo sapiens

<400> 834

atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccaggggtggg 60
 cagggattcg ccatccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
 accgttcata tgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
 ggcgacgag tccaacgctt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
 ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
 gcgcttaacg ggcacatcc cgggtgacgtc atctcgggtga cctggcaaac caagtcgggc 360
 ggcacgcgta cagggaaact gacattggcc gagggacccc cggccgaatt catgcacggg 420
 ccccaggtgc tggcaacgtg ctccgagtg gcttgcctg ccttggctgc cacctctgcg 480
 ggggtgcgtc tggagggggg ggaccggcca ccaaccttac ccagtcgaagg aagtggatgg 540
 ccatgttccc acagcctgag tggctgccac ctgatggctg atggagcaaa ggccttagga 600
 aaagcagatg gcccttggcc ctaccttttt gttagaagaa ctgatgttcc atgtcctgca 660
 gcgagtgagg ttggtggctg tgccccagc tcctggcgcg ccctcgaga ggtgactggg 720
 tgctctttgg gccctcttgg ccttgcccag catgcacaag cctcagtgct actactgtgc 780

310

tacaaatgga gccatatagg ggaaacgagc agccatctca ggagcaagggt gtatgctgcc 840
 ttggggggct ccagtccttg cctcaagggt cttatgtcac tgtgggcttc ttggttgc 900
 agaggcagac catag 915

<210> 835

<211> 304

<212> PRT

<213> Homo sapiens

<400> 835

Met	His	His	His	His	His	His	Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu
			5						10					15	
Ser	Gln	Gly	Gly	Gln	Gly	Phe	Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala
			20					25					30		
Ile	Ala	Gly	Gln	Ile	Lys	Leu	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala
		35					40					45			
Phe	Leu	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val
	50					55				60					
Gln	Arg	Val	Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr
65					70					75				80	
Gly	Asp	Val	Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr
				85					90					95	
Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser
			100					105					110		
Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	
		115					120					125			
Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Met	His	Gly	Pro	Gln	Val	Leu
		130				135					140				
Ala	Arg	Cys	Ser	Glu	Cys	Ala	Cys	Pro	Ala	Leu	Ala	Ala	Thr	Ser	Ala
145					150					155				160	
Gly	Val	Arg	Leu	Glu	Gly	Val	Asp	Arg	Pro	Pro	Thr	Leu	Pro	Ser	Gln
				165					170					175	
Gly	Ser	Gly	Trp	Pro	Cys	Ser	His	Ser	Leu	Ser	Gly	Cys	His	Leu	Met
		180						185					190		
Ala	Asp	Gly	Ala	Lys	Ala	Leu	Gly	Lys	Ala	Asp	Gly	Pro	Trp	Pro	Tyr
		195					200					205			
Leu	Phe	Val	Arg	Arg	Thr	Asp	Val	Pro	Cys	Pro	Ala	Ala	Ser	Glu	Val
		210				215					220				
Gly	Gly	Cys	Ala	Pro	Ser	Ser	Trp	Arg	Ala	Leu	Ala	Glu	Val	Thr	Gly
225					230					235				240	
Cys	Ser	Leu	Gly	Pro	Leu	Gly	Leu	Ala	Gln	His	Ala	Gln	Ala	Ser	Val
				245					250					255	
Leu	Leu	Leu	Cys	Tyr	Lys	Trp	Ser	His	Ile	Gly	Glu	Thr	Ser	Ser	His
		260						265					270		
Leu	Arg	Ser	Lys	Val	Tyr	Ala	Ala	Phe	Gly	Gly	Ser	Ser	Pro	Cys	Leu
		275					280					285			
Lys	Gly	Leu	Met	Ser	Leu	Trp	Ala	Ser	Trp	Leu	Ser	Arg	Gly	Arg	Pro
		290				295					300				

<210> 836

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 836

311

cgaagtcacg tggaggccag cctc

24

<210> 837

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 837

cctgaccgaa ttcattaact ggcctggac

29

<210> 838

<211> 166

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(166)

<223> Xaa = Any Amino Acid

<400> 838

Met	Gly	His	His	His	His	His	His	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg
1				5					10					15	
His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile
		20						25					30		
Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser
		35					40					45			
Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly
	50					55				60					
Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	Val
65					70				75					80	
Asn	Val	Ser	Val	Val	Ser	Glu	Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro
				85				90					95		
Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly	Gly	Gly	Gln	Xaa	Gln	Xaa
			100					105					110		
Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr
		115					120					125			
Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly
		130				135					140				
Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu
145					150				155						160
Lys	Thr	Val	Gln	Ala	Ser										
					165										

<210> 839

<211> 504

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(504)

<223> n = A,T,C or G

312

<400> 839
 atgggccatc atcatcatca tcacgtggag gccagcctct ccgtacggca cccagagtac 60
 aacagaccct tgctcgctaa cgacctcatg ctcatcaagt tggacgaatc cgtgtccgag 120
 tctgacacca tccggagcat cagcattgct tcgcagtgcc ctaccgcggg gaactcttgc 180
 ctcgtttctg gctgggggtct gctggcgaaac ggcagaatgc ctaccgtgct gcagtgcgtg 240
 aacgtgtcgg tgggtgtctga ggaggtctgc agtaagctct atgaccgcgt gtaccacccc 300
 agcatgttct gcgcggcgcg agggcaanac cagaangact cctgcaacgg tgactctggg 360
 gggcccctga tctgcaacgg gtacttgagc ggccttgtgt ctttcggaaa agccccgtgt 420
 ggccaagtgt gcgtgccagg tgtctacacc aacctctgca aattcactga gtggatagag 480
 aaaaccgtcc aggccagtta atga 504

<210> 840
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 840
 ctcagggttc cggagccgcg g 21

<210> 841
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 841
 ctatagaatt cattacaaaa aagctgggct ccagc 35

<210> 842
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 842
 Met Gln His His His His His Leu Arg Val Pro Glu Pro Arg Pro
 1 5 10 15
 Gly Glu Ala Lys Ala Glu Gly Ala Ala Pro Pro Thr Pro Ser Lys Pro
 20 25 30
 Leu Thr Ser Phe Leu Ile Gln Asp Ile Leu Arg Asp Gly Ala Gln Arg
 35 40 45
 Gln Gly Gly Arg Thr Ser Ser Gln Arg Gln Arg Asp Pro Glu Pro Glu
 50 55 60
 Pro Glu Pro Glu Pro Glu Gly Gly Arg Ser Arg Ala Gly Ala Gln Asn
 65 70 75 80
 Asp Gln Leu Ser Thr Gly Pro Arg Ala Ala Pro Glu Glu Ala Glu Thr
 85 90 95
 Leu Ala Glu Thr Glu Pro Glu Arg His Leu Gly Ser Tyr Leu Leu Asp
 100 105 110
 Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr Pro Lys
 115 120 125

313

Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln Val Ile
 130 135 140
 Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala Pro Glu
 145 150 155 160
 Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln Val Lys
 165 170 175
 Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln Leu Ser
 180 185 190
 Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala Leu Lys
 195 200 205
 Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn Ser Tyr
 210 215 220
 Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro Ala Phe
 225 230 235 240
 Trp

<210> 843
 <211> 729
 <212> DNA
 <213> Homo sapiens

<400> 843
 atgcagcatc accaccatca ccacctcagg gttccggagc cgcggcccgg ggaggcgaaa 60
 gcggaggggg ccgcgcgcgc gaccccgctc aagccgctca cgtccttctt catccaggac 120
 atcctgcggg acggcgcgca gcggcaaggc ggccgcacga gcagccagag acagcgcgac 180
 ccggagccgg agccagagcc agagccagag ggaggacgca gccgcgccgg gccgcagaaac 240
 gaccagctga gcaccgggccc ccgcgcgcgc ccggatgagg ccgagacgct ggcagagacc 300
 gagccagaaa ggcacttggg gtcttatctg ttggactctg aaaacacttc aggcgcctt 360
 ccaaggcttc cccaaacccc taagcagccg cagaagcgct cccgagctgc cttctccac 420
 actcaggtga tcgagttgga gaggaagttc agccatcaga agtacctgtc ggcccctgaa 480
 cgggcccacc tggccaagaa cctcaagctc acggagacc aagtgaagat atggttccag 540
 aacagacgct ataagactaa gcgaaagcag ctctcctcgg agctgggaga cttggagaag 600
 cactcctttt tgccggccct gaaagaggag gccttctccc gggcctccct ggtctccgtg 660
 tataacagct atccttacta cccatacctg cactgcgtgg gcagctggag cccagctttt 720
 tggtaatga 729

<210> 844
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 844
 ctactaagcg ctggagtgag ggatcag 27

<210> 845
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

314

<400> 845
catcgagaat tcactactct ctgactagat gtc

33

<210> 846
<211> 161
<212> PRT
<213> Homo sapiens

<400> 846
Met Gln His His His His His Ala Gly Val Arg Asp Gln Gly Gln
1 5 10 15
Gly Ala Arg Trp Pro His Thr Gly Lys Arg Gly Pro Leu Leu Gln Gly
20 25 30
Leu Thr Trp Ala Thr Gly Gly His Cys Phe Ser Ser Glu Glu Ser Gly
35 40 45
Ala Val Asp Gly Ala Gly Gln Lys Lys Asp Arg Ala Trp Leu Arg Cys
50 55 60
Pro Glu Ala Val Ala Gly Phe Pro Leu Gly Ser Asp Cys Arg Glu Gly
65 70 75 80
Gly Arg Gln Gly Cys Gly Gly Ser Asp Asp Glu Asp Asp Leu Gly Val
85 90 95
Ala Pro Gly Leu Ala Pro Ala Trp Ala Leu Thr Gln Pro Pro Ser Gln
100 105 110
Ser Pro Gly Pro Gln Ser Leu Pro Ser Thr Pro Ser Ser Ile Trp Pro
115 120 125
Gln Trp Val Ile Leu Ile Thr Glu Leu Thr Ile Pro Ser Pro Ala His
130 135 140
Gly Pro Pro Trp Leu Pro Asn Ala Leu Glu Arg Gly His Leu Val Arg
145 150 155 160
Glu

<210> 847
<211> 489
<212> DNA
<213> Homo sapiens

<400> 847
atgcagcatc accaccatca ccacgctgga gtgagggatc agggggcaggg cgcgagatgg 60
cctcacacag ggaagagagg gccctcctg cagggcctca cctgggccac aggaggacac 120
tgcttttcct ctgaggagtc aggagctgtg gatggtgctg gacagaagaa ggacagggcc 180
tggctcaggt gtccagaggc tgtcgtggc ttccctttgg gatcagactg cagggaggga 240
gggcggcagg gttgtggggg gaggatgacc tgggggtggc tccaggcctt 300
gccctgcct gggccctcac ccagcctccc tcacagtctc ctggccctca gtctctcccc 360
tccactccat cctccatctg gcctcagtg gtcattctga tccactgaact gaccataccc 420
agccctgccc acggccctcc atggctcccc aatgccctgg agaggggaca tctagtcaga 480
gagtagtga 489

<210> 848
<211> 132
<212> PRT
<213> Homo sapiens

<400> 848
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe

315

1	5	10	15
Ala Ile Pro	Ile Gly Gln Ala Met	Ala Ile Ala Gly Gln	Ile Arg Ser
	20	25	30
Gly Gly Gly	Ser Pro Thr Val His	Ile Gly Pro Thr	Ala Phe Leu Gly
	35	40	45
Leu Gly Val	Val Asp Asn Asn Gly	Asn Gly Ala Arg	Val Gln Arg Val
	50	55	60
Val Gly Ser	Ala Pro Ala Ala Ser	Leu Gly Ile Ser	Thr Gly Asp Val
	65	70	75
Ile Thr Ala	Val Asp Gly Ala Pro	Ile Asn Ser Ala	Thr Ala Met Ala
	85	90	95
Asp Ala Leu	Asn Gly His His Pro	Gly Asp Val Ile	Ser Val Asn Trp
	100	105	110
Gln Thr Lys	Ser Gly Gly Thr Arg	Thr Gly Asn Val	Thr Leu Ala Glu
	115	120	125
Gly Pro Pro	Ala		
	130		

<210> 849

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 849

ggggaattca tcacctatgt gccgcctctg c

31

<210> 850

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 850

gggctcgagt cactcgccca cgaaatccgt gtaaaacagc

40

<210> 851

<211> 1203

<212> DNA

<213> Homo sapiens

<400> 851

atgcacaccc	atcaccatca	caaggccgag	tccgataact	tccagctgtc	ccagggtggg	60
cagggattcg	ccattccgat	cgggcaggcg	atggcgatcg	cgggccagat	caagcttccc	120
accgttcata	tggggcctac	cgcccttcctc	ggcttgggtg	ttgtcgacaa	caacggcaac	180
ggcgacagag	tccaacgcgt	ggtcgggagc	gctccggcgg	caagtctcgg	catctccacc	240
ggcgacgtga	tcaccgcggt	cgacggcgct	ccgatcaact	cggccaccgc	gatggcggac	300
gcgcttaacg	ggcatcatcc	cggtgacgtc	atctcggtga	cctggcaaac	caagtcgggc	360
ggcacgcgta	cagggaacgt	gacattggcc	gagggacccc	cggccgaatt	catcacctat	420
gtgcccgcctc	tgctgctgga	agtgggggta	gaggagaagt	tcatgaccat	ggtgctgggc	480
attggtccag	tgctgggcct	ggtctgtgtc	cgcctcctag	gctcagccag	tgaccactgg	540
cgtggacgct	atggccgcgc	ccggcccttc	atctgggcac	tgtccttggg	catcctgtctg	600

316

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agcctctttc tcatccaag ggccggctgg ctagcagggc tgctgtgccc ggatcccagg 660
cccctggagc tggcactgct catcctgggc gtggggctgc tggacttctg tggccagggtg 720
tgcttcactc cactggaggc cctgctctct gacctcttcc gggacccgga ccactgtcgc 780
caggcctact ctgtctatgc ctcatgatc agtcttgggg gctgcctggg ctacctcctg 840
cctgccattg actgggacac cagtgccctg gccccctacc tgggcaccca ggaggagtgc 900
ctctttggcc tgctcacctt catcttcttc acctgcgtag cagccacact gctgggtggct 960
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ccccactgct gtccatgccg ggcccgttg gctttccgga acctgggcgc cctgcttccc 1080
cggctgcacc agctgtgctg ccgcatgccc cgcaccctgc gccggctctt cgtgggtgag 1140
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tga
1203

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<210> 852

<211> 400

<212> PRT

<213> Homo sapiens

<400> 852

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Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
          5          10          15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
          20          25          30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
          35          40          45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
          50          55          60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
          65          70          75          80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
          85          90          95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
          100          105          110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
          115          120          125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Thr Tyr Val Pro Pro Leu
          130          135          140
Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met Thr Met Val Leu Gly
          145          150          155          160
Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala
          165          170          175
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp
          180          185          190
Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala
          195          200          205
Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
          210          215          220
Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val
          225          230          235          240
Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro
          245          250          255
Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu
          260          265          270
Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser
          275          280          285
Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu
          290          295          300
Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala
          305          310          315          320

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Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala	Glu	Gly	Leu	Ser	Ala
				325				330						335	
Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg	Ala	Arg	Leu	Ala	Phe
				340				345						350	
Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His	Gln	Leu	Cys	Cys	Arg
				355			360							365	
Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala	Glu	Leu	Cys	Ser	Trp
				370		375								380	
Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr	Asp	Phe	Val	Gly	Glu
385					390					395					400

```

<400> 853
Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
                    5             10             15
Ser Val Arg Val
          20

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<400> 854
ctgctccac ctccaccgc gctctgcggg gcctctgcct gtgatgtctc cgtacgtgtg 60

<400> 855
Ala Ser Ala Cys Asp Val Ser Val Arg Val
 5 10

<400> 856
gcctctgcct gtgatgtctc cgtacgtgtg 30

<400> 857
Ala Ser Ala Cys Asp Val Ser Val Arg
1 5

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318

<211> 9
<212> PRT
<213> Homo sapiens

<400> 858
Ser Ala Cys Asp Val Ser Val Arg Val
5

<210> 859
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27

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<400> 861
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Met Val Leu

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<400> 862
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<400> 868
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320

<210> 869
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<212> PRT
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<400> 869
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<213> Homo sapiens

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<210> 875
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321

<213> Homo sapiens

<400> 875

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<210> 876

<211> 9

<212> PRT

<213> Homo sapiens

<400> 876

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<210> 877

<211> 9

<212> PRT

<213> Homo sapiens

<400> 877

Val Leu Val His Pro Gln Trp Val Leu
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<210> 878

<211> 1195

<212> DNA

<213> Homo sapiens

<400> 878

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<210> 879

<211> 339

<212> PRT

<213> Homo sapiens

322

<400> 879

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 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
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 Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
 65 70 75 80
 Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
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 Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
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 Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
 115 120 125
 Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
 130 135 140
 Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
 145 150 155 160
 Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
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 Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
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 Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
 195 200 205
 Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
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 Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
 225 230 235 240
 Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
 245 250 255
 Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
 260 265 270
 Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
 275 280 285
 Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
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 Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
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<211> 2172

<212> DNA

<213> Homo sapiens

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323

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<210> 881

<211> 2455

<212> DNA

<213> Homo sapiens

<400> 881

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<211> 2455

<212> DNA

<213> Homo sapiens

<400> 882

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325

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<210> 883

<211> 62

<212> PRT

<213> Homo sapiens

<400> 883

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              20              25              30
Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
              35              40              45
Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
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<210> 884

<211> 135

<212> PRT

<213> Homo sapiens

<400> 884

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              20              25              30
Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu
              35              40              45
Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu
              50              55              60
Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala
              65              70              75              80
Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly
              85              90              95
Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro
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Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile
              115              120              125
Leu Leu Asn Tyr Gln Val Ser
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<210> 885

<211> 77

<212> PRT

<213> Homo sapiens

<400> 885

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Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln

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326

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      20          25          30
Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro
      35          40          45
Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln
      50          55          60
Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu
      65          70          75

```

<210> 886

<211> 60

<212> PRT

<213> Homo sapiens

<400> 886

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Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
      20          25          30
Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
      35          40          45
Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
      50          55          60

```

<210> 887

<211> 76

<212> PRT

<213> Homo sapiens

<400> 887

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Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
          5          10          15
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
      20          25          30
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
      35          40          45
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
      50          55          60
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
      65          70          75

```

<210> 888

<211> 76

<212> PRT

<213> Homo sapiens

<400> 888

```

Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp
          5          10          15
Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu
      20          25          30
Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly
      35          40          45
Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
      50          55          60
Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
      65          70          75

```

327

<210> 889
 <211> 80
 <212> PRT
 <213> Homo sapiens

<400> 889
 Met Leu Leu His Ser Ser Leu Val Asn Arg Ala Arg Leu Cys Leu Lys
 5 10 15
 Asn Lys Gln Ile Asn Lys Gln Thr Asn Lys Thr Glu Arg Phe Cys Cys
 20 25 30
 Asn Val Gln Gly Ala Ile Cys Ser Phe Lys Lys Ile Ile Phe Gly Gln
 35 40 45
 Ala Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Ala Lys Val
 50 55 60
 Gly Gly Ser Phe Glu Val Arg Ser Leu Arg Ser Ala Trp Pro Thr Trp
 65 70 75 80

<210> 890
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 890
 Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro His Asn Pro
 5 10 15
 Ile Thr Ser His Gln Val Ser Ser Asp Thr Trp Asp Trp Val Gly Thr
 20 25 30
 Gln Ser Gln Thr Val Ser Asp Ala Ala Gly Ala Gly Asp Thr Glu Thr
 35 40 45
 Thr Gln Thr Trp Cys Leu Cys His Ser Ser Gly Leu Cys Leu Ser Pro
 50 55 60
 Gly Pro Pro Ser Pro Ser Met Val
 65 70

<210> 891
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 891
 Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln
 5 10 15
 Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His
 20 25 30
 Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro
 35 40 45
 Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln
 50 55 60
 Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu
 65 70 75

<210> 892
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 892

328

Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
 5 10 15
 Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
 20 25 30
 Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
 35 40 45
 Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
 50 55 60

<210> 893

<211> 76

<212> PRT

<213> Homo sapiens

<400> 893

Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
 5 10 15
 Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
 20 25 30
 Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
 35 40 45
 Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
 50 55 60
 Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
 65 70 75

<210> 894

<211> 2479

<212> DNA

<213> Homo sapiens

<400> 894

gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
 ctttgaactc aggggtcacca ccagctattg gaccttacta tgaaaacccat ggataccaac 120
 cggaaaaccc ctatcccgcga cagcccactg tgggtcccccac tgtctacgag gtgcatccgg 180
 ctcaagtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca 240
 accccgtcgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300
 agaaagcact gtgcatcacc ttgacctggt ggaccttccg cgtgggagct gcgctggccg 360
 ctggcctact ctggaagttc atgggagcga agtgctccaa ctctgggata gagtgcgact 420
 cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
 gggaggagcga gaatcgggtg gttcgctctt acggaccaa cttcatcctt cagatgtact 540
 catctcagag gaagtcctgg caccctgtgt gccaaagcga ctggaacgag aactacgggc 600
 gggcggcctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
 atgacagcgg atccaccagc tttatgaaac tgaacacaag tgccggcaat gtcgatatct 720
 ataaaaaact gtaccacagt gatgcctgtt cttcaaaagc agtggtttct ttacgctgtt 780
 tagcctgcgg ggtcaacttg aactcaagcc gccagagcag gatcgtgggc ggtgagagcg 840
 cgtccccggg ggcctggccc tggcaggtca gcctgcacgt ccagaacgtc cacgtgtgcg 900
 gaggtccat catcaccccc gagtggatcg tgacagccgc cactgcgtg gaaaaacctc 960
 ttaacaatcc atggcattgg acggcatttg cggggatttt gagacaatct ttcatgttct 1020
 atggagccgg ataccaagta caaaaagtga tttctcatcc aaattatgac tccaagacca 1080
 agaacaatga cattgcgctg atgaagctgc atgaagcctc gactttcaac gacctagtga 1140
 aaccagtgtg tctgcccac ccaggcatga tgctgcagcc agaacagctc tgctggattt 1200
 ccgggtgggg ggccaccgag gagaaagggg agacctcaga agtgctgaac gctgccaagg 1260
 tgctttcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac 1320
 cagccatgat ctgtgccggc ttcttgccag ggaacgtcga ttcttgccag ggtgacagtg 1380
 gagggcctct ggtcaacttc aacaacaata tctgggtggc gataggggat acaagctggg 1440
 gttctggctg tgccaaagct tacagaccag gagtgtacgg gaatgtgatg gtattcacgg 1500
 actggattta tcgacaaatg aaggcacaac gctaataccac atgggtcttcg tccttgacgt 1560

329

```

cgttttacaa gaaaacaatg gggctggttt tgcttccccg tgcattgattt actcttagag 1620
atgattcaga ggtcacttca tttttattaa acagtgaact tgtctggctt tggcactctc 1680
tgccatactg tgcaggctgc agtggctccc ctgcccagcc tgcctccctt aacccttgt 1740
ccgcaagggg tgatggccgg ctggttggtg gcactggcgg tcaattgtgg aaggaagagg 1800
gttgagggct gccccattg agatcttcct gctgagtcct ttccaggggc caattttgga 1860
tgagcatgga gctgtcactt ctcagctgct ggatgacttg agatgaaaaa ggagagacat 1920
ggaaagggag acagccaggt ggcacctgca gcggctgccc tctggggcca cttggtagtg 1980
tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagccctg 2040
gatggtggcc agaaataaag ggaccagccc ttcatgggtg gtgacgtggt agtcacttgt 2100
aaggggaaca gaaacatttt tgttcttatg gggtagaat atagacagtg cccttggtgc 2160
gaggggaagca attgaaaagg aacttgccct gagcactcct ggtgcaggtc tccacctgca 2220
cattgggtgg ggctcctggg agggagactc agccttcctc ctcatcctcc ctgaccctgc 2280
tcctagcacc ctggagagtg aatgcccctt ggtccctggc agggcgccaa gtttggcacc 2340
atgtcggcct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg 2400
atgctcagtt taaggtagac tgtttccatg ttatgtttct acacattgat ggtggtgacc 2460
ctgagttcaa agccattct 2479

```

<210> 895

<211> 492

<212> PRT

<213> Homo sapiens

<400> 895

```

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
      5      10      15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
      20      25      30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
      35      40      45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
      50      55      60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
      65      70      75      80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
      85      90      95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
      100     105     110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
      115     120     125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
      130     135     140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
      145     150     155     160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
      165     170     175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
      180     185     190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
      195     200     205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
      210     215     220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
      225     230     235     240
Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
      245     250     255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
      260     265     270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro

```

330

275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
 355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
 450 455 460
 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
 465 470 475 480
 Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
 485 490

<210> 896
 <211> 683
 <212> DNA
 <213> Homo sapiens

<400> 896
 gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
 ctttgaactc aggggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120
 cggaaaaccc ctatcccgcga cagcccactg tgggtcccccac tgtctacgag gtgcatccgg 180
 ctacgtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca 240
 acccgcgtgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300
 agaaagcact gtgcatcacc ttgaccctgg ggaccttccg cgtgggagct gcgctggccg 360
 ctggcctact ctggaagtgc atgggcagca agtgctccaa ctctgggata gagtgcgact 420
 cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
 gggaggacga gaatcgggtgt gttcgctctt acggacaaaa cttcatcctt cagatgtact 540
 catctcagag gaagtcctgg caccctgtgt gccaaagacga ctggaacgag aactacgggc 600
 gggcggcctg caggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
 atgacagcgg atccaccagc ttt 683

<210> 897
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 897
 Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
 1 5 10 15

331

Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
 20 25 30
 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe

<210> 898
 <211> 27
 <212> PRT
 <213> Homo sapiens

<400> 898
 Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr
 1 5 10 15
 Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
 20 25

<210> 899
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 899
 ggatccgccg ccaccatgct actttctagc ctgct

35

<210> 900
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 900

332

gtcgactcag ctggaccaca gccgcag

27

<210> 901

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 901

ggatccgccg ccaccatggg ctgcaggctg ctct

34

<210> 902

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 902

gtcgactcag aaatcctttc tcttgac

27

<210> 903

<211> 936

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...()

<223> n = A,T,C or G

<400> 903

```

atgggctgca ggctgntctg ctgtgcgggt ctctgtctcc tgggagcggg ccccatggaa 60
acgggagtta cgcagacacc aagacacctg gtcattggaa tgacaaataa gaagtctttg 120
aaatgtgaac aacatctggg tcataacgct atgtattggg acaagcaaag tgctaagaag 180
ccactggagc tcatgtttgt ctacagtctt gaagaacggg ttgaaaacaa cagtgtgcca 240
agtcgcttct cacctgaatg ccccaacagc tctcacttat tccttcacct acacaccctg 300
cagccagaag actcggccct gtatctctgc gccagcagcc aagaccggac aagcagctcc 360
tacgagcagt acttcgggcc gggcaccagg ctcacgggtca cagaggacct gaaaaacgtg 420
ttcccaccgg aggtcgtgtg gtttgagcca tcagaagcag agatctccca caccctaaaag 480
gccacactgg tgtgcctggc cacaggcttc taccctgacc acgtggagct gagctggtgg 540
gtgaatggga aggaggtgca cagtggggtc agcacagacc cgcagcccct caaggagcag 600
cccgcctca atgactccag atactgcctg agcagccgcc tgaggggtctc ggccaccttc 660
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcgagaaat 720
gacgagtgga cccaggatag ggccaaacct gtcacccaga tcgtcagcgc cgaggcctgg 780
ggtagagcag actgtggctt cacctccgag tcttaccagc aaggggtcct gtctgccacc 840
atcctctatg agatcttgct agggaaggcc accttgtagt ccgtgctggg cagtgccttc 900
gtgctgatgg ccatggtcaa gagaaaggat ttctga 936

```

<210> 904

<211> 834

<212> DNA

<213> Homo sapiens

333

<220>

<221> misc_feature

<222> (1)...()

<223> n = A,T,C or G

<400> 904

```

atgtcacttt cttagcctgct naaggtgggtc acagcttcac tgtggctagg acctggcatt 60
gccagaaga taactcaaac ccaaccagga atgttcgtgc aggaaaagga ggctgtgact 120
ctggactgca catatgacac cagtgatcaa agttatgggtc tcttctggta caagcagccc 180
agcagtgggg aaatgatttt tcttatttat caggggtctt atgacgagca aaatgcaaca 240
gaaggtcgct actcattgaa tttccagaag gcaagaaaat ccgccaacct tgtcatctcc 300
gcttcacaac tgggggactc agcaatgtat ttctgtgcaa tgagagaggg cgcgaggagg 360
ggaaacaaac tcacctttgg gacaggcact cagctaaaag tggaactcaa tatccagaac 420
cctgaccctg ccgtgtacca gctgagagac tctaaatcca gtgacaagtc tgtctgccta 480
ttcaccgatt ttgattctca aacaaatgtg tcacaaagta aggattctga tgtgtatata 540
acagacaaaa ctgtgctaga catgaggtct atggacttca agagcaacag tgctgtggcc 600
tggagcaaca aatctgactt tgcattgtgca aacgccttca acaacagcat tattccagaa 660
gacaccttct tccccagccc agaaagttcc tgtgatgtca agctgggtcga gaaaagcttt 720
gaaacagata cgaacctaaa ctttcaaaac ctgtcagtga ttgggttccg aatcctcctc 780
ctgaaagtgg ccgggtttaa tctgctcatg acgctgcggc tgtggtccag ctga 834

```

<210> 905

<211> 311

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(311)

<223> Xaa = Any amino acid

<400> 905

```

Met Gly Cys Arg Leu Xaa Cys Cys Ala Val Leu Cys Leu Leu Gly Ala
      5              10              15
Val Pro Met Glu Thr Gly Val Thr Gln Thr Pro Arg His Leu Val Met
      20              25              30
Gly Met Thr Asn Lys Lys Ser Leu Lys Cys Glu Gln His Leu Gly His
      35              40              45
Asn Ala Met Tyr Trp Tyr Lys Gln Ser Ala Lys Lys Pro Leu Glu Leu
      50              55              60
Met Phe Val Tyr Ser Leu Glu Glu Arg Val Glu Asn Asn Ser Val Pro
      65              70              75              80
Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser His Leu Phe Leu His
      85              90              95
Leu His Thr Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
      100             105             110
Ser Gln Asp Arg Thr Ser Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly
      115             120             125
Thr Arg Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu
      130             135             140
Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
      145             150             155             160
Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu
      165             170             175
Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
      180             185             190
Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
      195             200             205

```

334

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
 210 215 220
 Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
 225 230 235 240
 Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
 245 250 255
 Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr
 260 265 270
 Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
 275 280 285
 Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
 290 295 300
 Met Val Lys Arg Lys Asp Phe
 305 310

<210> 906

<211> 277

<212> PRT

<213> Homo sapiens

<400> 906

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
 5 10 15
 Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
 20 25 30
 Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
 35 40 45
 Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
 50 55 60
 Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
 65 70 75 80
 Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
 85 90 95
 Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
 100 105 110
 Ala Met Arg Glu Gly Ala Gly Gly Asn Lys Leu Thr Phe Gly Thr
 115 120 125
 Gly Thr Gln Leu Lys Val Glu Leu Asn Ile Gln Asn Pro Asp Pro Ala
 130 135 140
 Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
 145 150 155 160
 Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
 165 170 175
 Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
 180 185 190
 Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
 195 200 205
 Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
 210 215 220
 Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe
 225 230 235 240
 Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe
 245 250 255
 Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
 260 265 270
 Arg Leu Trp Ser Ser
 275

<210> 907
 <211> 1536
 <212> DNA
 <213> Homo sapiens

<400> 907
 atgtacaacc tgttgctgtc ctacgacaga catggggacc acctgcagcc cctggacctc 60
 gtgccaatc accagggctc caccctttc aagctggctg gaggaggagg taacactgtg 120
 atgtttcagc acctgatgca gaagcggag cacaccagtg ggacgtatgg accactgacc 180
 tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgctggaa 240
 cttatcatca ccaccaagaa gcgggaggct cgccagatcc tggaccagac gccggtgaag 300
 gagctgggtga gcctcaagtga gaagcggtag gggcgccgt acttctgcat gctgggtgcc 360
 atatatctgc tgtacatcat ctgcttcacc atgtgctgca tctaccgccc cctcaagccc 420
 aggaccaata accgcacgag ccccggggac aacacctctt tacagcagaa gctacttcag 480
 gaagcctaca tgacccttaa ggacgatatc cggctggctg gggagctggg gactgtcatt 540
 ggggctatca tcatcctgct ggtagagggt ccagacatct tcagaatggg ggtcactcgc 600
 ttctttggac agaccatcct tgggggccc ttccatgtcc tcatcatcac ctatgccttc 660
 atgggtgctgg tgaccatggg gatgcggctc atcagtcca gcggggagggt ggtaccatg 720
 tcctttgcac tcgtgctggg ctggtgcaac gtcagtact tcgcccagg attccagatg 780
 ctaggccctc tcaccatcat gattcagaag atgatttttg gcgacctgat gcgattctgc 840
 tggctgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
 gaggaccccc aggagctagg ccacttctac gactacccca tggccctgtt cagcaccttc 960
 gagctgttcc ttaccatcat cgatggccca gccaaactaca acgtggacct gcccttcatt 1020
 tacagcatca cctatgctgc ctttgccatc atcgccacac tgctcatgct caacctcctc 1080
 attgccatga tgggcgacac tcaactggca gtggcccatg agcgggatga gctgtggagg 1140
 gccagattg tggccaccac ggtgatgctg gagcggaagc tgcctcgtg cctgtggcct 1200
 cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
 gacaggcaag atctcaaccg gcagcggatc caacgctacg cacaggcctt ccacaccg 1320
 ggctctgagg atttggacaa agactcagtg gaaaaactag agctgggctg tcccttcagc 1380
 cccacctgt cccttcctat ccctcagtg tctcgaagta cctcccgag cagtggcaat 1440
 tgggaaaggc ttcggaagg gaccctgagg agagacctgc gtgggataat caacaggggt 1500
 ctggaggacg gggagagctg ggaatatcag atctga 1536

<210> 908
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 908
 atgtacaacc tgttgctgtc ctacgacaga catggggacc acctgcagcc cctggacctc 60
 gtgccaatc accagggctc caccctttc aagctggctg gaggaggagg taacactgtg 120
 atgtttcagc acctgatgca gaagcggag cacaccagtg ggacgtatgg accactgacc 180
 tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgctggaa 240
 cttatcatca ccaccaagaa gcgggaggct cgccagatcc tggaccagac gccggtgaag 300
 gagctgggtga gcctcaagtga gaagcggtag gggcgccgt acttctgcat gctgggtgcc 360
 atatatctgc tgtacatcat ctgcttcacc atgtgctgca tctaccgccc cctcaagccc 420
 aggaccaata accgcacgag ccccggggac aacacctctt tacagcagaa gctacttcag 480
 gaagcctaca tgacccttaa ggacgatatc cggctggctg gggagctggg gactgtcatt 540
 ggggctatca tcatcctgct ggtagagggt ccagacatct tcagaatggg ggtcactcgc 600
 ttctttggac agaccatcct tgggggccc ttccatgtcc tcatcatcac ctatgccttc 660
 atgggtgctgg tgaccatggg gatgcggctc atcagtcca gcggggagggt ggtaccatg 720
 tcctttgcac tcgtgctggg ctggtgcaac gtcagtact tcgcccagg attccagatg 780
 ctaggccctc tcaccatcat gattcagaag atgatttttg gcgacctgat gcgattctgc 840
 tggctgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
 gaggaccccc aggagctagg ccacttctac gactacccca tggccctgtt cagcaccttc 960
 gagctgttcc ttaccatcat cgatggccca gccaaactaca acgtggacct gcccttcatt 1020
 tacagcatca cctatgctgc ctttgccatc atcgccacac tgctcatgct caacctcctc 1080

336

```

attgccatga tgggcgacac tcaactggcga gtggcccatg agcgggatga gctgtggagg 1140
gccagattg tggccaccac ggtgatgctg gagcggaagc tgcctcgctg cctgtggcct 1200
cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
gacaggcaag atctcaaccg gcagcggatc caacgctacg cacaggcctt ccacaccccg 1320
ggctctgagg atttgacaa agactcagtg gaaaaactag agctgggctg tcccttcagc 1380
ccccacctgt cccttcctat gccctcagtg tctcgaagta cctcccgag cagtccaat 1440
tgggaaaggc ttcggcaagg gaccctgagg agagacctgc gtgggataat caacaggggt 1500
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```

<210> 909

<211> 511

<212> PRT

<213> Homo sapiens

<400> 909

```

Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
                    5              10              15
Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
          20              25              30
Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
          35              40              45
Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
          50              55              60
Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
          65              70              75              80
Leu Ile Ile Thr Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln
          85              90              95
Thr Pro Val Lys Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg
          100              105              110
Pro Tyr Phe Cys Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys
          115              120              125
Phe Thr Met Cys Cys Ile Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn
          130              135              140
Arg Thr Ser Pro Arg Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln
          145              150              155              160
Glu Ala Tyr Met Thr Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu
          165              170              175
Val Thr Val Ile Gly Ala Ile Ile Ile Leu Leu Val Glu Val Pro Asp
          180              185              190
Ile Phe Arg Met Gly Val Thr Arg Phe Phe Gly Gln Thr Ile Leu Gly
          195              200              205
Gly Pro Phe His Val Leu Ile Ile Thr Tyr Ala Phe Met Val Leu Val
          210              215              220
Thr Met Val Met Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met
          225              230              235              240
Ser Phe Ala Leu Val Leu Gly Trp Cys Asn Val Met Tyr Phe Ala Arg
          245              250              255
Gly Phe Gln Met Leu Gly Pro Phe Thr Ile Met Ile Gln Lys Met Ile
          260              265              270
Phe Gly Asp Leu Met Arg Phe Cys Trp Leu Met Ala Val Val Ile Leu
          275              280              285
Gly Phe Ala Ser Ala Phe Tyr Ile Ile Phe Gln Thr Glu Asp Pro Glu
          290              295              300
Glu Leu Gly His Phe Tyr Asp Tyr Pro Met Ala Leu Phe Ser Thr Phe
          305              310              315              320
Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro Ala Asn Tyr Asn Val Asp
          325              330              335
Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala Ala Phe Ala Ile Ala

```

337

```

      340      345      350
Thr Leu Leu Met Leu Asn Leu Leu Ile Ala Met Met Gly Asp Thr His
      355      360      365
Trp Arg Val Ala His Glu Arg Asp Glu Leu Trp Arg Ala Gln Ile Val
      370      375      380
Ala Thr Thr Val Met Leu Glu Arg Lys Leu Pro Arg Cys Leu Trp Pro
      385      390      395
Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly Leu Gly Asp Arg Trp Phe
      400      405      410      415
Leu Arg Val Glu Asp Arg Gln Asp Leu Asn Arg Gln Arg Ile Gln Arg
      420      425      430
Tyr Ala Gln Ala Phe His Thr Arg Gly Ser Glu Asp Leu Asp Lys Asp
      435      440      445
Ser Val Glu Lys Leu Glu Leu Gly Cys Pro Phe Ser Pro His Leu Ser
      450      455      460
Leu Pro Met Pro Ser Val Ser Arg Ser Thr Ser Arg Ser Ser Ala Asn
      465      470      475      480
Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg Arg Asp Leu Arg Gly Ile
      485      490      495
Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser Trp Glu Tyr Gln Ile
      500      505      510

```

<210> 910
 <211> 134
 <212> PRT
 <213> Homo sapiens

```

<400> 910
Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
      5      10      15
Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
      20      25      30
Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
      35      40      45
Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
      50      55      60
Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
      65      70      75      80
Leu Ile Ile Thr Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln
      85      90      95
Thr Pro Val Lys Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg
      100      105      110
Pro Tyr Phe Cys Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys
      115      120      125
Phe Thr Met Cys Cys Ile
      130

```

<210> 911
 <211> 55
 <212> PRT
 <213> Homo sapiens

```

<400> 911
Ala Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn Arg Thr Ser Pro Arg
      5      10      15
Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln Glu Ala Tyr Met Thr
      20      25      30
Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu Val Thr Val Ile Gly

```

338

35 40 45
 Ala Ile Ile Ile Leu Leu Val
 50 55

<210> 912
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 912
 Glu Val Pro Asp Ile Phe Arg Met Gly Val Thr Arg Phe Phe Gly Gln
 5 10 15
 Thr Ile Leu Gly Gly Pro Phe His Val Leu Ile Ile Thr Tyr Ala Phe
 20 25 30
 Met Val Leu Val Thr Met Val
 35

<210> 913
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 913
 Met Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met Ser Phe Ala
 5 10 15
 Leu Val Leu

<210> 914
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 914
 Gly Trp Cys Asn Val Met Tyr Phe Ala Arg Gly Phe Gln Met Leu Gly
 5 10 15
 Pro Phe Thr Ile Met Ile Gln Lys Met Ile Phe Gly Asp Leu Met Arg
 20 25 30
 Phe Cys Trp Leu Met Ala Val Val Ile Leu Gly Phe Ala Ser Ala Phe
 35 40 45
 Tyr Ile Ile Phe
 50

<210> 915
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 915
 Gln Thr Glu Asp Pro Glu Glu Leu Gly His Phe Tyr Asp Tyr Pro Met
 5 10 15
 Ala Leu Phe Ser Thr Phe Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro
 20 25 30
 Ala Asn Tyr Asn Val Asp Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala
 35 40 45
 Ala Phe Ala Ile Ile Ala Thr Leu Leu Met Leu Asn Leu Leu Ile Ala
 50 55 60
 Met Met Gly Asp Thr His Trp Arg Val Ala His Glu Arg Asp Glu Leu

339

65.		70		75		80									
Trp	Arg	Ala	Gln	Ile	Val	Ala	Thr	Thr	Val	Met	Leu	Glu	Arg	Lys	Leu
			85						90					95	
Pro	Arg	Cys	Leu	Trp	Pro	Arg	Ser	Gly	Ile	Cys	Gly	Arg	Glu	Tyr	Gly
		100						105					110		
Leu	Gly	Asp	Arg	Trp	Phe	Leu	Arg	Val	Glu	Asp	Arg	Gln	Asp	Leu	Asn
		115					120					125			
Arg	Gln	Arg	Ile	Gln	Arg	Tyr	Ala	Gln	Ala	Phe	His	Thr	Arg	Gly	Ser
		130					135				140				
Glu	Asp	Leu	Asp	Lys	Asp	Ser	Val	Glu	Lys	Leu	Glu	Leu	Gly	Cys	Pro
		145			150					155					160
Phe	Ser	Pro	His	Leu	Ser	Leu	Pro	Met	Pro	Ser	Val	Ser	Arg	Ser	Thr
			165					170						175	
Ser	Arg	Ser	Ser	Ala	Asn	Trp	Glu	Arg	Leu	Arg	Gln	Gly	Thr	Leu	Arg
			180					185					190		
Arg	Asp	Leu	Arg	Gly	Ile	Ile	Asn	Arg	Gly	Leu	Glu	Asp	Gly	Glu	Ser
		195					200					205			
Trp	Glu	Tyr	Gln	Ile											
		210													

<210> 916
 <211> 1302
 <212> DNA
 <213> Homo sapiens

<400> 916
 tggacaaagg ggggtcacaca ttccttccat acggttgagc ctctacctgc ctggtgetgg 60
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 ttcatcctaa taggcctccc tggtttagaa gaggtcagc tctggttggc cttcccattg 180
 tgctccctct accttattgc tgtgctaggt aacttgacaa tcactctacat tgtgcggact 240
 gagcacagcc tgcattgagcc catgtatata tttctttgca tgctttcagg cattgacatc 300
 ctcatctcca cctcatccat gcccaaaatg ctggccatct tctggttcaa ttccactacc 360
 atccagtttg atgcttgtct gctacagatg tttgccatcc actccttacc tggcatggaa 420
 tccacagtgc tgctggccat ggcttttgac cgctatgtgg ccatctgtca cccactgcgc 480
 catgccacag tacttacgtt gcctcgtgtc accaaaattg gtgtggctgc tgtgggtgcg 540
 ggggctgcac tgatggcacc ccttcctgtc ttcataaagc agctgccctt ctgccgctcc 600
 aatatccttt ccattccta ctgcctacac caagatgtca tgaagctggc ctgtgatgat 660
 atccgggtca atgtcgtcta tggccttacc gtcacatctc cggccattgg cctggactca 720
 cttctcatct cttctcata tctgcttatt ctttaagactg tgttgggctt gacacgtgaa 780
 gccaggcca aggcatttgg cacttgogtc tctcatgtgt gtgctgtgtt catattctat 840
 gtacctttca ttggattgtc catggtgcat cgcttttagca agcggcgtga ctctccgctg 900
 cccgtcatct tggccaatat ctatctgctg gttcctcctg tgcacaaccc aattgtctat 960
 ggagtgaaga caaaggagat tcgacagcgc atccttcgac ttttccatgt ggccacacac 1020
 gcttcagagc cctagggtgc agtgatcaaaa cttcttttcc attcagagtc ctctgattca 1080
 gattttaatg ttaacatttt ggaagacagt attcagaaaa aaaatttcct taataaaaaat 1140
 acaactcaga tccttcaa atgaaactgg ttggggaatc tccatttttt caatattatt 1200
 ttcttctttg ttttcttgct acatataatt attaataccc tgactagggt gtggtttgag 1260
 ggttattact tttcatttta ccatgcagtc caaatctaaa ct 1302

<210> 917
 <211> 2061
 <212> DNA
 <213> Homo sapiens

<400> 917
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 gtgtcagtga tcaaacttct tttccattca gagtcctctg attcagattt taatgttaac 120

atTTTggaag	acagtattca	gaaaaaaaaat	tTccttaata	aaaatacaac	tcagatcctt	180
caaatatgaa	actggTtggg	gaatctccat	TTTTTcaata	ttattttctt	ctttgttttc	240
ttgctacata	taattattaa	taccctgact	aggTtgtggt	tggagggtta	ttacttttca	300
ttttaccatg	cagtccaaat	ctaaactgct	tctactgatg	gtttacagca	ttctgagata	360
agaatggtac	atctagagaa	catttgccaa	aggcctaagc	acggcaaagg	aaaataaaca	420
cagaatataa	taaaatgaga	taatctagct	taaaactata	acttcctctt	cagaactccc	480
aaccacattg	gatctcagaa	aatgctgtc	ttcaaaatga	cttctacaga	gaagaaataa	540
tttttcctct	ggacactagc	acttaagggg	aagattggaa	gtaaagcctt	gaaaagagta	600
catttaccta	cgTtaatgaa	agtTgacaca	ctgttctgag	agttttcaca	gcatatggac	660
cctgtttttc	ctattttaatt	ttcttatcaa	ccctttaatt	aggcaaagat	attattagta	720
ccctcattgt	agccatggga	aaattgatgt	tcagtgggga	tcagtgaatt	aaatgggggtc	780
atacaagtat	aaaaattaaa	aaaaaaggac	ttcatgcca	atctcatatg	atgtggaaga	840
actgttagag	agaccaacag	ggtagtgggt	tagagatttc	cagagtctta	cattttctag	900
aggaggtatt	taatttcttc	tcactcatcc	agtgttgtat	ttaggaattt	cctggcaaca	960
gaactcatgg	ctttaatccc	actagctatt	gcttattgtc	ctggTccaat	tgccaattac	1020
ctgtgtcttg	gaagaagtga	tttctagggt	caccattatg	gaagattctt	attcagaaag	1080
tctgcatagg	gcttatagca	agtattttat	ttttaaaagt	tccatagggtg	attctgatag	1140
gcagtggagt	tagggagcca	ccagttagta	tgggaagtat	ggaatggcag	gtcttgaaga	1200
taacattggc	cttttgagt	tgactcgtag	ctggaaagt	agggaaatctt	caggaccatg	1260
ctttatttgg	ggctttgtgc	agtatggaac	agggactttg	agaccaggaa	agcaatctga	1320
cttaggcatg	ggaatcaggc	atttttgctt	ctgaggggct	attaccaagg	gttaataagg	1380
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aacatgtgat	catatatgtg	gtaagtttca	ttttcttttt	caatcctcag	gttccctgat	1500
atggattcct	ataacatgct	ttcatccctt	tttgtaatgg	atatcatatt	tggaatgcc	1560
tatttaatac	ttgtatttgc	tgctggactg	taagcccatg	agggcactgt	ttattattga	1620
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ctgtcctgaa	cacatagcca	ggcaattttt	cagccttctt	tgagttgggt	attattaaat	1800
tctggccatt	acttccaatg	tgagtggaag	tgacatgtgc	aatttctata	cctggctcat	1860
aaaaccctcc	catgtgcagc	ctttcatggt	gacattaaat	gtgacttggg	aagctatgtg	1920
ttacacagag	taaatcacca	gaagcctgga	tttctgaaaa	aactgtgcag	agccaaacct	1980
ctgtcatttg	caactccac	ttgtatttgt	acgaggcagt	tggataagtg	aaaaataaag	2040
tactattgtg	tcaagtctct	g				2061

<210> 918

<211> 957

<212> DNA

<213> Homo sapiens

<400> 918

atgatggTgg	atcccaatgg	caatgaatcc	agtgtctacat	acttcatcct	aataggcctc	60
cctggTtttag	aagaggctca	gttctgggtg	gccttcccat	tgtgtctccct	ctaccttatt	120
gctgtgctag	gtaacttgac	aatcatctac	attgtgcgga	ctgagcacag	cctgcatgag	180
cccatgtata	tatttctttg	catgctttca	ggcattgaca	tcctcatctc	caacctcatcc	240
atgccccaaa	tgctggccat	cttctgggtc	aattccacta	ccatccagtt	tgatgcttgt	300
ctgtctacaga	tgtttgccat	ccactcctta	tctggcatgg	aatccacagt	gctgctggcc	360
atggcttttg	accgctatgt	ggccatctgt	cacccactgc	gccatgccac	agtacttaag	420
ttgcctogtg	tcaccaaagt	tggtgtggct	gctgtgggtg	ggggggctgc	actgatggca	480
ccccttctctg	tcttcatcaa	gcagctgccc	ttctgcccgt	ccaatatcct	ttcccatcc	540
tactgcctac	accaagatgt	catgaagctg	gcctgtgatg	atatccgggt	caatgtcgtc	600
tatggcctta	tcgtcatcat	ctccgccatt	ggcctggact	cacttctcat	ctccttctca	660
tatctgctta	ttcttaagac	tgtgttgggc	ttgacacgtg	aagcccaggc	caaggcattt	720
ggcacttgog	tctctcatgt	gtgtgctgtg	ttcatattct	atgtaccttt	cattggattg	780
tccatgggtgc	atcgctttag	caagcggcgt	gactctccgc	tgcccgtcat	cttggccaat	840
atctatctgc	tggttcctcc	tgtgctcaac	ccaattgtct	atggagtga	gacaaaggag	900
attogacagc	gcatecttcg	acttttccat	gtggccacac	acgcttcaga	gccctag	957

<210> 919

341

<211> 954

<212> DNA

<213> Homo sapiens

<400> 919

```

atgatggtgg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctggtttag aagagggtca gttctggttg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccatgtata tatttctttg catgctttca ggcattgaca tctcatctc cacctcatcc 240
atgccccaaa tgctggccat cttctggttc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcctttg accgctatgt ggccatctgt caccactgc gccatgccac agtacttacg 420
ttgcctcgtg tcacaaaaat tgggtgtggct gctgtggtgc ggggggctgc actgatggca 480
ccccttcctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttccatttcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggccctggact cacttctcat ctccttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtaccttt cattggattg 780
tccatggtgc atcgcttttag caagcggcgt gactctccgc tgcccgatc cttggccaat 840
atctatctgc tggttcctcc tgtgctcaac ccaattgtct atggagtga gacaaaggag 900
attcgacagc gcacccctcg acttttccat gtggccacac acgcttcaga gccc 954

```

<210> 920

<211> 318

<212> PRT

<213> Homo sapiens

<400> 920

```

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
                    5                      10                      15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
                20                      25                      30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
                35                      40                      45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
                50                      55                      60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
                65                      70                      75                      80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
                85                      90                      95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
                100                     105                     110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
                115                     120                     125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
                130                     135                     140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
                145                     150                     155                     160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
                165                     170                     175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
                180                     185                     190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
                195                     200                     205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
                210                     215                     220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
                225                     230                     235                     240

```

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Gly	Thr	Cys	Val	Ser	His	Val	Cys	Ala	Val	Phe	Ile	Phe	Tyr	Val	Pro
				245					250					255	
Phe	Ile	Gly	Leu	Ser	Met	Val	His	Arg	Phe	Ser	Lys	Arg	Arg	Asp	Ser
			260					265						270	
Pro	Leu	Pro	Val	Ile	Leu	Ala	Asn	Ile	Tyr	Leu	Leu	Val	Pro	Pro	Val
			275				280							285	
Leu	Asn	Pro	Ile	Val	Tyr	Gly	Val	Lys	Thr	Lys	Glu	Ile	Arg	Gln	Arg
	290					295					300				
Ile	Leu	Arg	Leu	Phe	His	Val	Ala	Thr	His	Ala	Ser	Glu	Pro		
305					310					315					

```
<210> 921
<211> 28
<212> PRT
<213> Homo sapiens
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<400> 921
Met Met Val Asp Pro Asn Gly Asn Glu5 Ser Ser Ala Thr Tyr Phe Ile
Leu Ile Gly Leu Pro Gly Leu Glu10 Glu Ala Gln Phe
Leu Ile Gly Leu Pro Gly Leu Glu15 Glu Ala Gln Phe
Leu Ile Gly Leu Pro Gly Leu Glu20 Glu Ala Gln Phe
Leu Ile Gly Leu Pro Gly Leu Glu25 Glu Ala Gln Phe

```

```
<210> 922
<211> 9
<212> PRT
<213> Homo sapiens
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<400> 922
Arg Thr Glu His Ser Leu His Glu Pro
5

```
<210> 923
<211> 21
<212> PRT
<213> Homo sapiens
```

```

<400> 923
Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp
                    5              10              15
Ala Cys Leu Leu Gln
              20

```

```
<210> 924
<211> 20
<212> PRT
<213> Homo sapiens
```

```

<400> 924
Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu
                    5              10              15
Thr Leu Pro Arg
                20

```

```
<210> 925
<211> 37
<212> PRT
<213> Homo sapiens
```

343

<400> 925

Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser
 5 10 15
 Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg
 20 25 30
 Val Asn Val Val Tyr
 35

<210> 926

<211> 13

<212> PRT

<213> Homo sapiens

<400> 926

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<210> 927

<211> 10

<212> PRT

<213> Homo sapiens

<400> 927

Val His Arg Phe Ser Lys Arg Arg Asp Ser
 5 10

<210> 928

<211> 22

<212> PRT

<213> Homo sapiens

<400> 928

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<210> 929

<211> 3245

<212> DNA

<213> Homo sapiens

<400> 929

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<210> 930
 <211> 1479
 <212> DNA
 <213> Homo sapiens

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345

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<210> 931

<211> 1476

<212> DNA

<213> Homo sapiens

<400> 931

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<210> 932

<211> 492

<212> PRT

<213> Homo sapiens

<400> 932

346

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 20 25 30
 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Ser Asn Phe Ile Leu Gln Val
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
 355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
 450 455 460

347

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
 465 470 475 480
 Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
 485 490

<210> 933
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 933
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 20 25 30
 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu
 100

<210> 934
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 934
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 20 25 30
 Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn Arg
 35 40 45
 Cys Val Arg Leu Tyr Gly Ser Asn Phe Ile Leu Gln Val Tyr Ser Ser
 50 55 60
 Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Trp Asn Glu Asn
 65 70 75 80
 Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe Tyr
 85 90 95
 Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met Lys
 100 105 110
 Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr His
 115 120 125
 Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile Ala
 130 135 140
 Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly Gly
 145 150 155 160
 Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His Val
 165 170 175
 Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp Ile
 180 185 190

348

Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp His
 195 200 205
 Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr Gly
 210 215 220
 Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp Ser
 225 230 235 240
 Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro Leu
 245 250 255
 Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly Met
 260 265 270
 Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala Thr
 275 280 285
 Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val Leu
 290 295 300
 Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn Leu
 305 310 315 320
 Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val Asp
 325 330 335
 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn Asn
 340 345 350
 Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala Lys
 355 360 365
 Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp Trp
 370 375 380
 Ile Tyr Arg Gln Met Arg Ala Asp Gly
 385 390

<210> 935
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 935
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22

<210> 936
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 936
 cgtgaactcg agtcattaga ttaacctcgt ggacgc

36

<210> 937
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

349

<400> 937
gtgctgtggg agtccccgcg gc

22

<210> 938
<211> 1158
<212> DNA
<213> Homo sapiens

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<210> 939
<211> 1020
<212> DNA
<213> Homo sapiens

<400> 939
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<210> 940
<211> 336

350

<212> PRT

<213> Homo sapiens

<400> 940

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Thr Asn Thr Cys Lys Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr
                35                40                45
Val Thr Cys Val Cys Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val
                50                55                60
Cys Gly Ser Asn Gly Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln
                65                70                75                80
Ala Ala Cys Lys Gln Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser
                85                90                95
Cys Ala Thr Asp Ala Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly
                100                105                110
Ser Gly Glu Thr Ser Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln
                115                120                125
Phe Gly Ala Glu Cys Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys
                130                135                140
Asn Ile Asp Cys Ser Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp
                145                150                155                160
Gly Lys Ser Tyr Asp Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln
                165                170                175
Lys Gln Glu Lys Ile Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn
                180                185                190
Thr Thr Thr Thr Thr Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp
                195                200                205
Tyr Ala Glu Asn Ala Asn Lys Leu Glu Glu Ser Ala Arg Glu His His
                210                215                220
Ile Pro Cys Pro Glu His Tyr Asn Gly Phe Cys Met His Gly Lys Cys
                225                230                235                240
Glu His Ser Ile Asn Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly
                245                250                255
Tyr Thr Gly Gln His Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val
                260                265                270
Val Pro Gly Pro Val Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile
                275                280                285
Gly Thr Ile Gln Ile Ala Val Ile Cys Val Val Val Leu Cys Ile Thr
                290                295                300
Arg Lys Cys Pro Arg Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr
                305                310                315                320
Gly His Tyr Ser Ser Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
                325                330                335

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<210> 941

<211> 381

<212> PRT

<213> Homo sapiens

<400> 941

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                20                25                30

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351

Pro Val Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe
 35 40 45
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<211> 15

<212> PRT

<213> Homo sapiens

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Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys Val Asn
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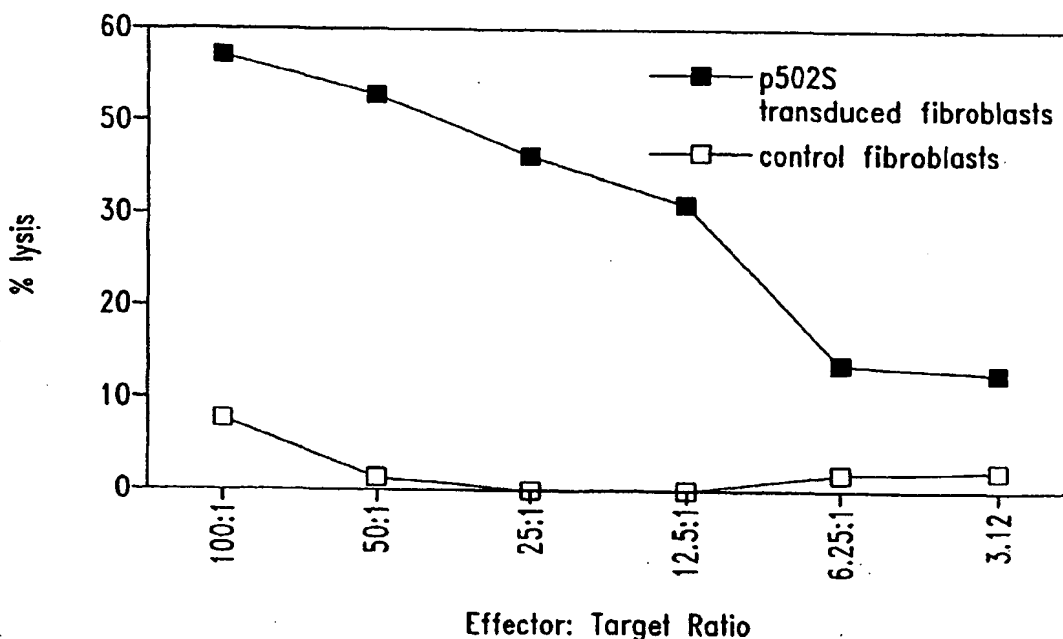
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09/657,279	6 September 2000 (06.09.2000)	US

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly prostate cancer, are disclosed. Illustrative compositions comprise one or more prostate-specific polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly prostate cancer.

WO 01/073032 A3



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(74) Agents: POTTER, Jane, E., R.; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 et al. (US).

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LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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INTERNATIONAL SEARCH REPORT

Inter ... lication No
PCT/US 01/09919

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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E	WO 01 34802 A (HARLOCKER SUSAN L ; CORIXA CORP (US); DAY CRAIG H (US); JIANG YUQIU) 17 May 2001 (2001-05-17) claims 31-55 ---	9-17
E	WO 01 51633 A (FANGER GARY RICHARD ; HARLOCKER SUSAN L (US); MEAGHER MADELEINE JOY) 19 July 2001 (2001-07-19) claims -----	1-17

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/09919

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 9 12 13 and 17 are (partially) directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-17 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-17 partially

Polynucleotide with SEQ ID NO 1, the encoded polypeptide, antibodies against the polypeptide and their uses

Inventions 2-651: claims 1-17 partially

Polynucleotides with SEQ ID NO's selected from 2-942 as mentioned in claim 1, the encoded polypeptides, antibodies against the polypeptides and their uses

INTERNATIONAL SEARCH REPORT

 Into
 PCT/US 01/09919⁷

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